

## STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 99448

TO: Karen A Lacourciere

Location: CM1/11D09/11E12

**Art Unit: 1635** 

Friday, July 25, 2003

Case Serial Number: 08765244

From: Susan Hanley

**Location: Biotech-Chem Library** 

CM1 6B05

Phone: 305-4053

susan.hanley@uspto.gov

Search Notes			
		·	*
	•		
·			





# STIC SEARCH RESULTS FEEDBACK FORM

#### **Biotech-Chem Library**

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

/O)	Untary Results Feedback Form
<b>&gt;</b>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
,	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
<b>A</b>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Coi	mments:

Drop of or send completed forms to STIGIBlotech-Chem Library CMil - Circ. Desk



#### STIC-Biotech/ChemLib

From:

Sent: To:

Lacourciere, Karen Tuesday, July 22, 2003 5:29 PM STIC-Biotech/ChemLib sequence search request 08/765,244

Subject:

JUL 23 2003

Please search SEQ ID NO:1 and 22 in the amino acid databases for 08/765,244. Thank-you!

Karen A. Lacourciere Ph.D. CM1 11D09 GAU 1635 (703) 308-7523

Searcner:	
Phone:	
Location:	
Date Picked Up:	
Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:
outer

/ENDOR/COST (where applic.)	
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (coesifu)	

```
GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 21:59:18; Search time 36.119 Seconds

(without alignments)

180.176 Million cell updates/sec

180.176 Million cell updates/sec

Sequence: US-08-765-244-1

Sequence: LBLOSUM62

Gapop 10.0, Gapext 0.5

Searched: L107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum Match 10%

Post-processing: Minimum Match 10%

Listing first 45 summaries
```

Database :

1. SIDSI/goddata/geneseq/geneseqp-embl/AA1980.DAT:\*
2. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
3. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
4. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
5. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
6. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
7. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
8. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
9. SIDSI/goddata/geneseq/geneseqp-embl/AA1980.DAT:\*
11. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
12. SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
13. SIDSI/goddata/geneseq/geneseqp-embl/AA1991.DAT:\*
14. SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
15. SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
16. SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
17. SIDSI/goddata/geneseq/geneseqp-embl/AA1999.DAT:\*
18. SIDSI/goddata/geneseq/geneseqp-embl/AA1999.DAT:\*
19. SIDSI/goddata/geneseq/geneseqp-embl/AA1999.DAT:\*
20. SIDSI/goddata/geneseq/geneseqp-embl/AA1999.DAT:\*
21. SIDSI/goddata/geneseq/geneseqp-embl/AA1999.DAT:\*
22. SIDSI/goddata/geneseq/geneseqp-embl/AA1999.DAT:\*
23. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
24. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
25. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
26. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
27. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
28. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
29. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
21. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
22. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
23. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
24. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
25. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
26. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*
27. SIDSI/goddata/geneseq/geneseqp-embl/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Rat ornithine tran	Rat ornithine tran	Human ornithine tr	Protein encoded by	OTC peptide fragme	Mitochondrial matr	Mitochondrial matr	Localisation seque	Mitochondrial matr
ID	AAR90584	ABG30857	ABG30856	AAB18445	AAG64224	AAR48260	AAW96358	ABG92993	ABP56588
DB	17	23	23	21	22	15	20	23	54
Length	43	32	32	258	32	32	35	32	32
% Query re Match Length DB ID	94.7	76.4	51.9	51.9	50.5	44.2	44.2	44.2	44.2
Score	197	159	108	108	105	92	85	92	92
Result No.		2	m	4	S	9	7	80	σ

ial ma	oug	acte	hul	S. cerevisiae DNA	Neisseria meningit	Neisseria meningit	Arabidopsis thalia	Salmon pleopiomela	Drosophila melanog	Drosophila melanog	Human protease and	Human polypeptide	Dipeptidyl peptida	Human DPP8 524Phe-	Human dipeptidyl p	Human DPP8 318Thr-	Human vesicle tran	vesicle	Amino acid sequenc		human	human		DPP8.	Human dipeptidyl p	Human DPPIV relate	prote	acid se	Human serine prote	Human ORFX protein					
AAB1570	1 AAB2283	0 AAY0493	2 AAU2346	2 AAB4671	1 AAY7546	1 AAY7546	1 AAG0415	1 AAG0415	7	1 AAG3758	1 AAG2619	1 AAG3758	AAP5063	2 ABB6417	2 ABB5925	2 AAB7467	3 ABB8973	3 ABB99	2 AAB4718	3 ABB0899	2 AAB4718	0 AAY5012	0 AAW7070	2 AAB3156	2 AAB9356	3 ABB9736	3 ABB9736	2 ABB5774	2 AAB4718	3 AAE2417	3 ABG6159	3 AAU7474	3 AAG7841	4 ABU0772	3 ABP0223
31 2	_1	'n	o.		8	80	0	3	e	m	o	و	S	و	'n	و	m	0	0	0	ß	8	<u>س</u>	8	01	4	a	vo	~	~	a	ď	C)	~	ហ
38.2		7	<u>.</u>	9	ė.	ė.	4	4	4	4	4	4.	4.	4	4.	4.	4.	4.	4	4.	4.	4.	₹.	4.	4.	4.	4.	4.	4.	4	4.	4	₹.	4	m.
9	٠	S	5	Š.	4.	4.	ä	Ή.	51.5	Ή.	÷.	÷.	S	50.5	ö	20	20	20	20	20	50	20	20	50	20	20	20	20	20	50	50	20	20	20	49.5
10	11	12	13	14	15	16	17	18	19									28															43	44	45

### ALIGNMENTS

ō

ó

Gaps

ö

ö

Length 32; Indels

```
The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a furansfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence of a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism. The present sequence represents the signal peptide of human mitochondrial confithine transcarbamylase (MOT) which may be used in the vector of the
          The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism. The present sequence represents the signal peptide of rat mitochondrial ornithine transcarbamylase (MOT) which may be used in the vector of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A recombinant vector for expressing a fused protein, useful decomposing an extranuclear gene of a nonhuman organism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ornithine transcarbamylase; MOT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; signal peptide; ornithine transcarbamylase; MOT recombinant vector; fusion protein; extranuclear gene.
                                                                                                                                                                                                                                                                                                          core 159; DB 23;
Pred. No. 8.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 108; DB 23;
Pred, No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ornithine transcarbamylase signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                                                                                                                                                                                                                                      1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                                                                                                                                       76.4%; Score 159; DB 100.0%; Pred. No. 8.6 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TANA/) TANAKA M.
(GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 3; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG30856 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-2000; 2000JP-0380975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-2000; 2000JP-0380975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-569946/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK88418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2002176988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-2002.
                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG30856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG30856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *888888888
                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                  Two modified oligonucleotides (introducing PstI and XhoI sites) were used to amplify a region of the human mitochondrial (mt) genome contg. the light strand promoter, mtDNA ori of the heavy strand, CSB's ("conserved sequence blocks") and a regulation site for DNA replication. Sequence blocks") and a requiation site for DNA replication. Estimated this fragment (5' direction) a synthetic multiple cloning site was introduced, generating a product with overhanign ends. The synthetic region also introduced a bidirectional mt transcription termination sequence. The amplification product, synthetic fragment and pBluescript were ligated and recombinant plasmid (AATI315) was produced. Human mt 16S rRNA (differing from the native RNA only in having a modified nuclectide) was isolated by PCR from chloramphenical resistant HeLa cloned insert was isolated as a BasI fragment and cyclised using haripin loop oligonuclectides, one of which carried the required signal peptide (the present sequence). The cyclised product was purified by treatment with exonuclease III. In a modification, the signal peptide was attached after cyclisation. The new plasmids were able to impart chloramphenicol resistance to otherwise sensitive B lymphocytes and fibroblasts. Similar plasmids without a signal peptide could not do this. The plasmids can be introduced into eukaryotic cells, esp. for site-directed mutagenesis or molecular therapy of genetic diseases, targetting nucleic acid in cells or their organales via the protein transport route.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A recombinant vector for expressing a fused protein, useful for decomposing an extranuclear gene of a nonhuman organism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDLC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; ornithine transcarbamylase; MOT; vector; fusion protein; extranuclear gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 197; DB 17;
Pred. No. 1.1e-23;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat ornithine transcarbamylase signal peptide.
  and molecular therapy of genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TANA/) TANAKA M.
(GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
                                              Disclosure; Column 11; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 3; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG30857 standard; Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.78;
95.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-2000; 2000JP-0380975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-2000; 2000JP-0380975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 95.3
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-569946/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK88419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2002176988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; signal recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG30857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
```

a ö

ö

Gaps

ö

Indels Length

32;

RESULT 4

ğ a

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR48260 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                    AAG64224 standard; Peptide; 32
                                                                                                                     51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.5%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0330631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0330631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTC peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-395263/42.
                                                                                                                                       Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                             Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 AA;
                                                                             258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2001145493-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mar.
Local Sim-
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR48260;
                                                                                                                                                                                                                                                                                                                                                                                                 AAG64224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                Sequence
                                                                                                                     Query Match
Best Local
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                    AAG64224
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DXXXEE
888888
                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ğ
                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a method for functionally complementing one or more defects, mutations, or deletions in a mitochondrial genome of a cell having a nuclear genome. The method is used for treating a disease or disorder that arises from deletion of the protein-encoding genes of a disorder that arises from one or more defects, deletions or mutations in mitochondrial genes encoding ribosomes or tRNA for transcription and translation in the mitochondrial encephalmyopathy with carboards and stroke-like episodes. Leber hereditary optic lactic acidosis and stroke-like episodes, Leber hereditary optic neuropathy, myoclonic epilepsy with ragged-red fibres, neurogenic concurpathy, myoclonic epilepsy with ragged-red fibres, neurogenic concurpathy, myoclonic epilepsy with ragged-red fibres, neurogenic concurpathy, myoclonic epilepsy with ragged-red fibres, neurogenic associated deafness, diabetes with deafness, leukodystrophy with hypodycemia, autism with seizures, sudden infant death syndrome with hypodycemia, leukaemia with maternally inherited thrombocytopenia, multiple sclerosis with seizures, blindness with optic atrophy and controlic, renal tubilar acidosis with elevated lactic acid and hypotonia, convalvular hypertrophic cardiomyopathy before age 50 and chronic convalvular hypertrophic cardiomyopathy before age 50 and chronic convalutis with stroke-like episodes. The present sequence is encoded by plasmid puoshrey comparises a mutant oligomycin-
                                                                                                                                                                                                                                                                                                 Mitochondrial genome; mitochondrial encephalmyopathy; lactic acidosis; Leber hereditary optic neuropathy; myoclonic epilepsy; neurogenic muscular weakness; ataxia; retinitis pigmentosa; kearns-Sayre syndrome; Leigh syndrome; Dearson Marrow pancreas syndrome; aminody.ycoside-associated deafness; diabetes; deafness; leukodystrophy; hypotonia; autism; sudden infant death syndrome; hypoglycemia; leukaemia; hybotopia, migranhe; hearing loss; stroke, refractory infantile reflux; carnitine deficiency; multiple sclerosis; blindness; optic atrophy; renal tubular acidosis; cardiomyopathy; chronic pancreatitis; ATPase 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or deletions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functionally complementing one or more defects, mutations, or deletions in a mitochondrial genome of a cell, useful for treating dlabetes with deafness, comprises introducing mitochondrial DNA into the nuclear
1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
                      || |||||||| || || || ||||||| ||:||:|
1 MLFNLKILLNNAAFRNGHNFWVRNFRCGQPLQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                Ş
                                                                                                                                                                                                                                                                        Protein encoded by plasmid pUOATP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3; 49pp; English.
                                                                                                                                            AAB18445 standard; Protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US06037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0123336.
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zullo SJ, Eisenstadt JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-565602/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA75084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200053773-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1999;
                                                                                                                                                                                                                                15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                      AAB18445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qenome
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for preparing a protein which interacts with the heat shock protein HSP47. The method involves the two-hybrid screening method using the HSP47 gene and a mammalian cDMA library. The HSP47 interacting proteins are useful for the diagnosis and treatment of diseases caused by an increase or decrease in activity of HSP47. The present sequence was used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                             Gaps
resistant ATPase 6 mitochondrial gene derived from Chinese hamster (CHO) cells linked to ornithine transcarbamylase DNA sequence. It used for targeting the protein to the mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Using the two-hybrid screening method to prepare proteins which interact with the heat shock protein \mbox{HSP47}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                             ó
                                                                                                                                                         Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shock protein interacting protein; HSP47; OTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105; DB 22;
Pred. No. 3.3e-09;
2; Mismatches 8;
                                                                                                                                                         21;
                                                                                                                                                                                                             8;
                                                                                                                                                            Score 108; DB 21;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                 Pred. No. 1.46
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 12; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ
```

```
Expressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMA), so that the expression of multiple major histocompatibility (MHC) contact the expression of multiple major histocompatibility (MHC) contact his solective targeting of IRMS, their pathways or components, can be used to selectively regulate the immune system by controlling expression of these molecules and preventing an undesired immune response in a cell. Any component of the MHC pathway or the MHC assembly line or antigen presentation can be targeted. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for transplantation can be perfixed with the intrabody ex vivo. The intrabodies can comprise whole antibodies, heavy chains, Fab. fragments, single-chain antibodies, and diabodies. The intrabodies and intracellular localisation signal to facilitate interception of expressed proteins. For example, if the target was a cell surface receptor, the antibody would comprise a leader sequence and an endoplasmic reticulum (ER) or Golgi apparatus mitochondrial matrix. For other localisation sequences for the mitochondrial matrix. For other localisation sequences for the mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Altering the regulation of the immune system
                                                                                                                                               /note= "Any amino acid"
32
                                                                                                                                                                                                       /note= "Any amino acid"
                                                                                                                      /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                     (DAND ) DANA FARBER CANCER INST INC.
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 28; 56pp; English.
                                                                                                                                                                                                                                                                                                                                    98WO-US19563.
                                                                                                                                                                                                                                                                                                                                                                          97US-0059339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marasco W, Mhashikar A;
  endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-229546/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 AA;
                                                                                                                                          Misc-difference
                                                                                                                                                                                     Misc-difference
                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                  18-SEP-1998;
                                                                                                                                                                                                                                                 WO9914353-A2
                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2002
                                                                                                                                                                                                                                                                                          25-MAR-1999
                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG92993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG92993
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vector systems comprise a sequence adapted for intracellular delivery and expression contq. a promoter operably linked to an antibody gene encoding an antibody which binds to a specific target antigen. The antibody is esp, a single chain antibody in which the heavy and light chain variable regions are joined via a hydrophilic linker peptide. Localisation sequences are pref. included in the constructs. The sequence AAR48260 is a mitochondrial matrix retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intracellular binding of antigens - by using antibody targetting with vector system, for e.g. tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; immune response; modulation; MHC; IRM; receptor; intrabody; major histocompatibility complex; graft rejection; immunomodulatory response molecule; regulation; transplantation, retention signal; localisation signal; golgi apparatus; ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                   Single chain antibody, sFv; heavy chain; light chain; variable domain; hydrophilic linker; antibodies; targetting; subcellular localisation signal; mitochondrial matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrial matrix localisation signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92; DB 15;
Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
               Mitochondrial matrix retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 103; 155pp; English.
                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                           'note= "not defined"
                                                                                                                                                                                                                                                                                     'note= "not defined'
                                                                                                                                                                                                                                                                                                                              /note= "not defined"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW96358 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-US06735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0916939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marasco WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-048868/06.
                                                                                                                                                                                                                                                                                                          Misc-difference 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 AA;
                                                                                                                    retention signal
                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haseltine WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                      WO9402610-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-1994
                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW96358
```

```
ö
                                             Gaps
                                           ô
                                                                                                                                                                                                                                                                                                                                                                 Localisation sequence to direct antibodies to the mitochondria.
Length 32;
                                           Indels
44.2%; Score 92; DB 20; L
61.3%; Pred. No. 3.9e-07;
Live 2; Mismatches 10;
                                                                                   1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                   MLFNLRXXLNNAAFRHGHNFMVRNFRCGOPL 31
                                                                                                                                                                                                                                    ABG92993 standard; Peptide; 32 AA
```

δ a 31

1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGOPL 1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV

```
The invention discusses a mechanic for another properties encoding a regulator polypeptide, whose expression induces activation of a target transcriptional regulatory region in a host cell. The method comprises providing a population of eukaryotic host cell. The method comprises polypeptide, introducing into the host cell a library of polypuclectides and the recovering them from the host cell a library of polypuclectides and then recovering them from the host cells. The target transcriptional regulatory region is operably associated with a polypuclectide encoding a gene product, the expression of which results in host cell death or cause the host cells to exhibit a pre-determined modified phenotype and where the gene product is expressed upon activation of target transcriptional regulatory region. Each candidate regulator polypeptide comprises a condidate peptide is displayed on the surface of the candidate regulator regulatory region the surface of the candidate regulator molecules, such as polypeptides, which directly or indirectly induce or suppress the transcriptional activation of a target transcriptional regulatory region in a eukaryotic host cell. These regulator molecules may be used (e.g. in gene therapy) for preventing or transcriptional regulatory region in a eukaryotic host cell. These cegulator molecules may be used (e.g. in gene therapy) for preventing or treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases (e.g. Alzhelmer's disease), bone pathologies, dermachologie (e.g. arrhythmia, heart failure, ischaemia), obesity, neurodegenerative diseases (e.g. Alzhelmer's disease), bone pathologies, dermachologic diseases (e.g. alzhelmer's disease), bone pathologies, dermachologic consultations and in molecules that consultations and in wound consultations and in improving the performance of existing or esistance applications and in improving the performance of existing or alloring transport mechanisms, in drug toxicities and dermanications and in higherholes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention discloses a method for identifying polynucleotides encoding
                 Regulator; transcription; cell death; phenotype; molecular scaffold; gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure; ischemia; obesity; neurodegenerative disease; Alzhehmer's disease; bone pathology; dermatologic disease; psoriasis; infection; AIDS; acquired immunodeficiency syndrome; cosmettc; wound healing; antibiotic transport; drug toxicity; drug resistance; immunobiology; inflammation; allergic response; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic response and in biotechnology applications. The sequences presented in ABG92946-ABG93029 are examples of regulator polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying regulator polypeptides which influence target transcriptional regulatory regions, useful for treating cancer, comprises introducing host cells expressing the polypeptide into library of polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 37; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-265880P.
2001US-271423P.
2001US-263226P.
2000US-192586P.
97US-935377P.
                                                                                                                                                                                                                                                                                                                                                                                                             2001US-265589P
                                                                                                                                                                                                                                                                                                                                                              2002WO-US02814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRP ) UNIV ROCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-643398/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 AA;
                                                                                                                                                                                                                                                                WO200262822-A2
                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                            04-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                             32-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2000;
22-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2001;
27-FEB-2001;
                                                                                                                                                                                                                                                                                                                15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sauderer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
```

q

```
The present invention describes a method for selecting polynucleotides (PNS) encoding an intracellular immunoglobulin molecule or its fragment whose expression induces a modified phenotype in a eukaryotic host cell (I). The method comprises introducing into (I) a first and second ilbrary of PNS encoding, through operable association with a transcriptional control region, first and second intracellular immunoglobulin subunit polypeptides, respectively. The method is useful for selecting polynucleotides which encode an intracellular immunoglobulin molecule, or fragment. The method is useful e.g. for identifying polynucleotides which singly or collectively encode intracellular immunoglobulin molecules, or which sensitise host cells to killing by an agent. The method may also be used in cardiowascular applications; for screening for diminished arrhythmia potential in cardiomycytes and for enhanced contractile properties of cardiomycytes and diminish heart fallure potential; for identifying intracellular immunoglobulin molecules that will regulate intracellular and sarcolemmal calcium cycling in cardiomycytes to prevent arrhythmias or that will diminish embolic phenomena in arteries
                                                                                                                                                                                    Identification; intrabody; eukaryotic cell; immunoglobulin; selection; cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke; enhanced contractile property; heart failure; arrhythmia; embolic; sarcolemmal calcium cycling; artery; arteriole; angina; atherosclerosis; LDL metabolism; skin biology; keloid formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selecting polynucleotides encoding an intracellular immunoglobulin which induces a modified phenotype in a enkaryotic host cell, by introducing ilbrary of polynucleotides encoding immunoglobulin subunit polypeptides
                                                                                                                                                  Mitochondrial matrix targeting peptide SEQ ID NO:54.
                                                                                                                                                                                                                                                                                                                                                                           /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                               'note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UYRP ) UNIV ROCHESTER MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 44; 257pp; English
                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
                                      Ą
                                    ABP56588 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-263225P.
2001US-263200P.
2001US-271422P.
2001US-298095P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-2002; 2002WO-US01677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-103408/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei C,
                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200286096-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JAN-2001;
24-JAN-2001;
                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-JUN-2001;
                                                                                                              24-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zauderer M,
                                                                        ABP56588;
                    ABP56588
RESULT
```

ö

Gaps

ö

44.2%; Score 92; DB 23; Length 32; 61.3%; Pred. No. 3.9e-07; ive 2; Mismatches 10; Indels

Best Local Similarity 61.3 Matches 19; Conservative

Seguence Query Match therapy for the treatment of disorders such as Alzheimer's disease.

ï

```
ö
and arterioles leading to strokes and angina; in screening for decreases in atherosclerosis-producing mechanisms to find intracellular immunoglobulin molecules that regulate LDL and HDL metabolism; in skin biology applications; and in regulating or inhibiting keloid formation. ABZ22379 to ABZ22449 and ABPS6536 to ABPS6618 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  direct stabilised single-chain antibodies to the mitochondrial matrix. The N-terminus of the single-chain antibodies to the mitochondrial matrix fusion peptide, referred to as a tabilon, which increases stability of the antibody against proteclysis in vivo. Degradation of the antibody may be modulated by linking the stabilon to the antibody through a protesse-sensitive linker region. The stabilon is removed upon induction of a specific restriction protesse by means of an inducible promoter, and this renders the antibody susceptible to proteclysis by the N-end rule pathway. This method for regularing protein stability allows removal of the antibody after it has bound to its target antigen. Stabilised recombinant proteins may be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stabilon; stabilising fusion peptide; vaccine; gene therapy;
protein degradation modulation; protein stability; Alzhelmer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating degradability of protein or peptide useful for gene therapy involving antibodies, comprises altering a gene at the N terminus to render protein or peptide metabolically stable -
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a localisation sequence that can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix localisation sequence; single-chain antibody;
                                                                                                                                                                                                  ;
                                                                                                                                                                Length 32;
                                                                                                                                                                                                10; Indels
                                                                                                                                                            44.2%; Score 92; DB 24;
61.3%; Pred. No. 3.9e-07;
ive 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "unspecified amino acid"
                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                         1. MLFNLRXXLNNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MIND-) MINDSET BIOPHARMACEUTICALS USA INC. (MCIN/) MCINNIS P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrial matrix localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 50; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                     AAB15704 standard; Peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0115505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2000; 2000WO-US00558
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-476059/41
                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                          32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200042185-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-2000.
                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                         AAB15704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chain DG;
                                                                                                                                                                                                                                                                                                                     RESULT 10
AAB15704
888888888
                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                              qq
```

```
The invention relates to a controlled release drug delivery system.

Target cells in a patient are transformed with an expression construct encoding an antibody (particularly a single chain antibody) to the drug to be delivered. The antibody contains a modulator of intracellular half-life; this can either be a stabilising or destabilising residue located in the N-terminus after the initial methionine, or a peptide ("stabilon") containing a stabilising residue linked to the antibody N-terminus via a protease cleavage site. On administration of the drug, the antibody binds the drug, localising it at the target cells but maintaining it in an inactive state. As the antibody is degraded (the timescale for which is dependent upon the N-terminal or stabilon amino acides), the drug is released at its site of action where it can exert its effects. The antibody encoded by the expression construct (and therefore the therapeutic agent) can be targetted to particular therapeutic agent) can be targetted to particular cellular localisation signals. The novel method may be used to deliver therapeutic agents with a variety of conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                                      Controlled release delivery system; drug targetting; dudg-specific antibody; intracellular half-life; gene therapy; diabetes; autoimmune disease; inflammatory disease; infectious disease; cancer; side effect; subcellular localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delivering a drug, to a patient suffering from cancer or diabetes, at a predetermined site, comprises altering a target cell to express a drug specific antibody by gene therapy and administering the drug
                                                                                                             Gaps
                                                                                                             ij
                                                                          Length
                                                                                                             Indels
                                                                      Score 79.5; DB 21;
Pred. No. 3.6e-05;
1; Mismatches 10;
                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                            1 MLFNLR-XLNNAAFRHGHNFWYRNFRCGGPL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MIND-) MINDSET BIOPHARMACEUTICALS USA INC
                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrial matrix localisation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 44; 69pp; English.
                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= unknown
                                                                                                                                                                                                                                                                         AAB22835 standard; peptide; 31
                                                                    Query Match 38.2%;
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000; 2000WO-US04749
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-572044/53.
                                     31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200050089-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                  10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-2000.
                                     Sequence
                                                                                                                                                                                                                                                                                                               AAB22835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chain DG;
                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                          AAB22835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
8 X G
                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                               õ
```

ö

Gaps

. 0

Indels

13;

7; Mismatches

13; Conservative

```
Matches
                                                                                                                                       AAU23468
                                                                             g
                                                   δ
dispetes, autoimmune diseases, inflammatory diseases, infectious diseases and especially cancer. The delivery method of the invention causes a drug to become almost immediately localised at its site of action in an inactive form where it accumulates. Once released by antibody degradation, the drug is at an effective concentration only at the target site, with very little free drug being available in the rest of the body. The system of the invention therefore reduces the side effects caused by therapeutic agents, and also provides economic benefits as a smaller amount can be administered to the patient. Sequences AAB22835, AAB22837 and AAB228397 represent subcellular localisation sequences which can incorporated into a drug-specific antibody used in the method of the invention.
                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   χ,
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goguet de la Salmoniere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                             Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 165; 0.73;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying coding or promoter sequences involved infection-associated protein expression
                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                          38.2%; Score 79.5; DB 21
61.3%; Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim EM, Pelicic V, Portnoi D,
                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium species protein sequence 38B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterial DNA vectors containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                             AAY04933 standard; Protein; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32; Fig 38B; 309pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.9%;
39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-FR01813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97FR-0011325
97FR-0010404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                        Similarity 61.3
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-181045/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 AA;
                                                                                                                                                                                                              31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX34186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9909186-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guigueno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gicquel B,
                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY04933;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                AAY0493
                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; inflammatory disorder; inflammatory disorder; inflammatory disorder; informational disorder; informational disorder; nephrotropic; anticoagulant.
          38
6 RILLNKAALRKAHTSMVRNFRYGKPVQSQLKPR
                                                                                                                         Novel human enzyme polypeptide #554.
                                                                   Ā
                                                                  AAU23468 standard; Protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0216880.
2000US-0217487.
2000US-0217496.
                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01239
                                                                                                                                                                                                                                                                                                                                   2000US-0189874
                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0218290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20000S-0224518
20000S-0224519
                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0216647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0225214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0225758
                                                                                                         (first entry)
                                                                                                                                                                                                                                   WO200155301-A2.
                                                                                                                                                                                                                                                                                                                                16-MAR-2000;
17-MAR-2000;
19-MAR-2000;
19-MAR-2000;
20-JUN-2000;
20-JUN-2000;
20-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000;
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2000;
                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                      02-AUG-2001
                                                                                     AAU23468;
```

```
05-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0230437.
08-SEP-2000; 2000US-0231443.
08-SEP-2000; 2000US-0231443.
08-SEP-2000; 2000US-0231444.
14-SEP-2000; 2000US-0231968.
14-SEP-2000; 2000US-0231968.
14-SEP-2000; 2000US-0231969.
15-SEP-2000; 2000US-0231999.
16-SEP-2000; 2000US-0231999.
16-SEP-2000; 2000US-0231999.
17-SEP-2000; 2000US-0231999.
13-CCT-2000; 2000US-0241199.
13-CCT-2000; 2000US-0246519.
13-CCT-2000; 2000US-0249511.
13-CCT-2000; 2000US-0249211.
13-CCT-2000; 2000US-0249211.
13-CCT-2000; 2000US-0249211.
13-CCT-2000; 2000US-0249211.
13-CCT-2000; 2000US-0249211.
```

```
The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wider range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIDE) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. arthritis), neurologi 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LRILLNK----AALRKAHTSMVRNFRYG-----KPVQSQL---KPR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.7%; Score 55.5; DB 22; Length 149; Best Local Similarity 35.3%; Pred. No. 1.6; Matches 18; Conservative 6; Mismatches 10; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID No 1464; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC, Ruben SM;
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-0251986.
05-DEC-2000; 2000US-0251986.
05-DEC-2000; 2000US-0251866.
06-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-465566/50.
N-PSDB; AAS41338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
AAB46718
ID AAB46
XX
AC AAB46
         q
```

AAB46718 standard; Protein; 761 AA

AAB46718;

```
Neisseria meningitidis ORF 715 protein sequence SEQ ID NO: 2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-062150/05
N-PSDB; AAZ54227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 AA;
                                                                                                                                                                                    W09957280-A2
                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                30-APR-1999;
                                                                                                                                                                                                                                    11-NOV-11999
                                                                                                                                                                                                                                                                                                                             01-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
    NAMES OF COLORS OF THE STREET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel isolated nucleic molecule (I) comprising the genome of bacteriophage RM 378. The invention also describes (I) an isolated nucleic acid which encodes a polypeptide obtainable from bacteriophage RM 378 (II); (3) a DNA construct (III) comprising operatively linked to a regulatory sequence; (4) a host cell comprising (III); and (5) an isolated polypeptide (IV) obtainable from (II) its active derivative or fragment. Bacteriophage RM 378 is useful for active derivative or fragment absteriophage RM 378 is useful for producing thermophilic enzymes useful in DNA research and commercial settings (e.g. proteases and lipses used in washing powder, hydrolytic enzymes useful in the manufacture of encoded polypeptide, as probes continue of host cells. The polypeptides can be used as a molecular species), as well as for detecting the presence of the bacteriophage in a culture of host cells. The polypeptides can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns. Because the host organism of the RM378 bacteriophage is a thermophile, the enzymes and proteins of that RM378 bacteriophage are significantly more thermostable than those of other (e.g. mesophilic) columns their use under temperature conditions which would be prohibitive content enzymes, thus increasing the range of conditions which can be employed not only in DNA research but also in commercial settings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid from bacteriophage RM 378 encoding enzymes useful
In recombinant DNA technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hjorleifsdottir S, Hreggvidsson GO, Fridjonsson OH, Aevarsson A;
Kristjansson JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 MPNLRCLSLSIQTLMNPKENKQEIVSITLSAYRNISLDSPIPENIKPDDLC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LSNLRILL------NKAALRKAHTSMVRNFRYGKPVQSQLKPRDLC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 761;
                                                                     S. cerevisiae DNA polymerase protein fragment SEQ ID NO 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                             Genome; thermophilic enzyme; washing powder; bleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.7%; Score 55.5; Dilarity 29.4%; Pred. No. 12; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Figure 3A-P; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY75465 standard; Protein; 138
                                                                                                                                                                                                                                                                                                 02-JUN-2000; 2000WO-IB00893.
                                                                                                                                                                                                                                                                                                                                                 99US-0137120
                                                                                                                                                                                                                                                                                                                                                                                                (DECO-) DECODE GENETICS EHF
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                              Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Local 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-061727/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761 AA;
                                                                                                                                                                                                        WO200075335-A2.
                                                                                                                                                                                                                                                                                                                                                 12-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000
                                                                                                                                                                                                                                                       14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY75465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AAY75465
ID AAY75
XX
AC AAY75
XX
DT 21-MA
XX
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
```

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N gonorrhaea polynucleotides and polypeptides. AA25457 to AA254576 and AA254616 to AA25473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also have use as antibacterial agents. The polynucleotides of the invention may also be used to screen for agonists or antagonists, which may themselves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Σ
Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.5; DB 21;
Pred. No. 2.1;
4; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 RILLNKAALRKAHTSMVRNFRY-GKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 RYLLMRRLSETMHTAVKLNFRYAGRPKWVGLKYRD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: July 24, 2003, 22:04:07 Job time : 38.119 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 1154; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C, Galeotti C, Grandi G, 1
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.2%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                         98US-0083758.
98US-0094869.
98US-009994.
98US-0103749.
98US-0103794.
98US-0103796.
                                                                                                                                                                                                                                                                                                    99WO-US09346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.2
Best Local Similarity 42.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                                                          Neisseria meningitidis
```

```
9, Appli
4, Appli
18053, A
30808, A
30808, A
50808, A
5110, Appli
6, Appli
6, Appli
6, Appli
7, Appli
8, Appli
8, Appli
8, Appli
8, Appli
9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREDILT 1-190-29

US-06-373-190-29

Sequence 29, Application US/08373190

STREET INVENTION: MATHOR METHOD OF INTRACELLULAR BINDING OF PROTEINS

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSEE: USK, MERONETEN, ROBERTS & CUSHMAN

CITY: BOSTON

CONTRY: MA

COUNTRY: MA

COU
                                          sednence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32,
US-09-328-352-7632
US-08-903-1199B-9
US-08-903-1199B-9
US-09-428-711A-4
US-09-252-91A-18053
US-09-252-91A-30808
US-09-428-711A-2
US-09-428-711A-2
US-09-428-711A-2
US-09-428-711A-19085
US-09-252-991A-19085
US-09-428-711A-14
US-09-914-259-68
US-09-914-259-68
US-09-914-259-68
US-09-608-810A-5
US-09-608-810A-5
US-09-608-810A-5
US-09-608-810A-5
US-09-457-708-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.28;
       444

\(\Omega\) 44444

\(\dagga\) \(\dagga\)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
           Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 27, Appl
Sequence 32812, Appl
Sequence 3391, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 25705, Appl
Sequence 25705, Appl
Sequence 296.33, Appl
Sequence 296.34, Appl
Sequence 27, Appl
Sequence 2, Appl
Sequence 3, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                        July 24, 2003, 22:02:54; Search time 20.0119 Seconds (without alignments) 86.686 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-765-244-1
208
1 MLSNLRILLNKAALRKAHTS......VRNFRYGKPVQSQLKPRDLC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-373-190-29
US-08-438-190A-29
US-08-438-190A-29
US-09-287-145A-29
US-09-556-111-29
US-09-556-111-29
US-09-252-911A-32812
US-09-252-911A-32812
US-09-252-911A-32812
US-09-34-476-1
US-09-314-476-1
US-09-314-476-1
US-09-314-476-1
US-09-314-476-1
US-09-318-811-2
US-09-732-210-98
US-09-732-210-195
US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š.
```

```
RESULT 4
US-09-287-145A-29
US-09-287-145A-29
Sequence 29, Application US/09287145A
Fatent No. 6072036
GENERAL INFORMATION:
APPLICANT: MARSECO, WAINE
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESSE:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: QUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: Patentin Pc-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: EISRNSTEIN, ROMALD I.
REGISTRATION: 310628
REFERENCE/DOCKET NUMBER: 41956-CP3
REPERBENCE/DOCKET NUMBER: 41956-CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-6440
TELEPHONE: (617) 523-6440
TELERA: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,145A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 3;
Pred. No. 1.3e-07;
2; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUSHMAN
CITY: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
OMPUTER F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTORNEY/AGENT INFORMATION
    MASSACHUSETTS
US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                         02109
                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                    ·;
                        Gaps
                                                                                           RESULT 2
US-08-438-190A-29
Sequence 29, Application US/08438190A
Sequence 29, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
APPLICANT: HASELITIE, WILLIAM
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCE: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. COLLIN; DIKE, BRONSTEIN, ROBERTS G. ADDRESSEE: CUSHANA
STREET: 130 WATER STREET
CITT: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-350-215-29
Sequence 29, Application US/08350215
Sequence 20, Application US/08350215
Sequence 20, Application US/08350215
Sequence 20, Application
Sequence 20, Application
Sequence 30000000
SEQUENCE OF SEQUENCES
SEQUENCES: 58
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUSHMAN
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 32;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
FILING DATE:
61.3%; Pred. No. 1.3e-07; tive 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; Score 92; DB 2;
llarity 61.3%; Pred. No. 1.3e-07;
Conservative 2; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFRENCE/DOCKET NUMBER: 4195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELERAX: (617) 523-3400
TELERAX: (617) 523-3400
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 32 amino acids
amino acid
GY: linear
Best Local Similarity 61.39
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-438-190A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                ő
```

ó

0; Gaps

```
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 32812
LENGTH: 457
                                                                                  APPLICANT:
                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/09556111
Patent No. 6329173
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
APPLICANT: MARASCO, WAILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 92; DB 4; Length 32;
Pred. No. 1.3e-07;
2; Mismatches 10; Indels
                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                             Score 92; DB 3;
Pred. No. 1.3e-07;
2; Mismatches 10
                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                            1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGOPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,111
FILING DATE: 21-APr-2000
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: BOSTON
STATE: MASSACHUSETTS
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cn 44.2%;
l Similarity 61.3%;
19; Conservative 2
                                                                                                                                             Ouery Match
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserval
                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                              US-09-287-145A-29
                                                                                                                                                                                                                                                                                                            US-09-556-111-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-556-111-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE DO INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEC ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (451)

, OTHER INFORMATION: Identity of amino acid at the above locations are unknown.

US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 MPNLRCLSLSIQTLANPKENKQEIVSITLSAYRNISLDSPIPENIKPDDLC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LSNLRILL------NKAALRKAHTSMVRNFRYGKPVQSQLKPRDLC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                         APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bocteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bocteriophage RM378 of a Thermophilic
TITLE OF INVENTION: 2739.1001-001
CURRENT APPLICATION NUMBER: US/09/585,858
CURRENT FILING DATE: 2000-12-18
PRIOR PAPLICATION NUMBER: 60/137,120
PRIOR PAPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
25.0%; Score 52; DB 4; Length 457;
Best Local Similarity 34.4%; Pred. No. 6.3;
Matches 11; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: | : | : |
176 VALDAAVRRARLVRFRGFRLGRPAQLYVETR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ILLNKAALRKAHTSMVRNFRYGKPVQSQLKPR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55.5; D. Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 32812, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5399, Application US/09107532A Patent No. 6583275
                                                                                    Sigridur Hjorleifsdotter
Gudmundur O. Hreggyldsson
Olafur H. Fridjonsson
Sequence 27, Application US/09585858; Patent No. 6492161; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae US-09-585-858-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.7%;
ilarity 29.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-09-107-532A-5399
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 593;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 NLRILLINKAALRKAHTSMVRNFRY-----GKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW VESICLE TRANSPORT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,927
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/900,927
FILING DATE: FILED HEREWITH
APPLICATION NUMBER: STILING DATE:
RIGHT SATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: BF-0350 US
TELEPHONE: 415-85-0555
TELEPHONE: 415-85-0555
                                                                                                DB 4;
8.2;
                                                                                             Score 50; DB Pred. No. 8.2; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.0%; Score 50; DB Best Local Similarity 31.1%; Pred. No. 18; Matches 14; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                        17 AHTSMVRNF -- RYGKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08900927
Patent No. 5840537
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: COLley, Neil C.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NEW VESICLE THE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence 1, Application US/09191279; Sequence No. 5981192; Patent No. 5981192; GENERAL INFORMATION: APPLICANT: Bandman, Olga
                                                                                                24.0%;
                                                                                             Query Match
Best Local Similarity 44.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
      ; ORGANISM: Homo sapiens US-09-794-236-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: MMLR20T01
CLONE: 475485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-900-927-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-900-927-1
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    å
                         APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09794236

Patent No. 6337069

GENERAL INFORMATION:
APPLICANT: Grouzmanh, Eric
APPLICANT: Lacroix, Jean-Silvain
APPLICANT: Mond, Michel
TILLE OF INVENTION: Method of Treating Rhinitis and Sinusitis
FILE REFERENCE: 81986/276823
CURRENT FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 310

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٠.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: CD
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51.5; D
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.8%; Score 51.5; I
llarity 44.4%; Pred. No. 2.9;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc_feature

; LOCATION: (B) LOCATION 1...208

; SEQUENCE DESCRIPTION: SEQ ID NO: 5399:

US-09-107-532A-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 NKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 NKAA------ONFRYGKPFTPELE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5399:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserva:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-794-236-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           å
```

```
RESULT 13
US-09-252-91A-25705
Sequence 25705, Application US/09252991A
Sequence 25705, Application US/09252991A
Patent No. 6511795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
TITLE OF INVENTION: NUMBER: US 60/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1999-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-252-991A-29653
Sequence 29653, Application US/09252991A
Sequence 29653, Application US/09252991A
Sequence 29651795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:||| |: || 496 AAVREAHAGMLFDWIRGIKRRTTISNAEIDLRGQAFRYGEPEGGRLVP 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RNFRYGKPVQSQLKP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 4; Length 547;
Pred. No. 23;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NLRILLNKAALRKAHTSMVRNFRY------GKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER:
PPLING DATE:
ATTONINE/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-035
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEDRIONE: 415-85-0555
"TILEPRAK: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AALRKAHTSMV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25705
                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPER: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.6%; 27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.0%;
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.6
Best Local Similarity 27.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: MMLR20T01
CLONE: 475485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 25705
LENGTH: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-334-476-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.0%; Score 50; DB 2; Length 593; Best Local Similarity 31.1%; Pred. No. 18; Matches 14; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 NLAKLIQHANV-QAHSSLIRNLEQLGGTVTNPGGSGTSSRLEPRE 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NIRILLINKAALRKAHTSMVRNFRY------GKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09334476
Patent No. 6162901
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
TITLE OF INFORMATION: NW VESICLE TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inoque Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                           APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
TILLE OF LAVORTION: NEW VESICLE TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           OURPUTER: LEW COMPACIANTE OPERATING SYSTEM: DOS CURRAIT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/191,279
FILING DATE:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/900,927
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0350 US
TELEROMAUNICATION INFORMATION:
TELEROMAUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OFFWARE: Fastseg for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,476
                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto COUNTRY: USA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845.4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LIBRARY: MMLR20T01
; CLONE: 475485
US-09-191-279-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Pa]
STATE: C!
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-334-476-1
```

q ŏ

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08428488

Patent No. 5524894
GENERAL INFORMATION:
MICHOLAS S.
TITLE OF INVENTION:
FILL OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
BUINS, Doane, Swecker & Mathis
STREET: Po. Box 1404
COMPITE: Virginia
STREET: Virginia
STREET: Po. Dox 1404
COMPITE: Virginia
STREET: Po. Dox 1404
COMPITE: Virginia
STREET: Virginia
STREET: Po. Dox 1404
COMPITE: Virginia
STREET: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 30
OTHER INFORMATION: /note= "Position 30 = Glu-NH2."
US-08-428-488-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 39
OTHER INFORMATION: /note= "Position 39 = Phe-OH."
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "Position 1 = H-Ser."

FRATURE:

NAME/KEY: Modified-site

LOCATION: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                  Score 48.5; DE; Pred. No. 12; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 AALRTQRVDALRNFQQG-PVQAAEQP 203
PRIOR APPLICATION NUMBER: US 60/074,789
PRIOR FILING DATE: 1998-02-18
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 274
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AALRKAHTSMVRNFRYGKPVQSQLKP 37
                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29653
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.3%;
Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
Query Match
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 22 VRNFRYGRPVGSQLKP 37
::|||||| ::|
Db 4 MEHFRYGRRVGKRRP 19
Search completed: July 24, 2003, 22:08:52
Job time: 21.0119 secs
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

July 24, 2003, 22:02:24 ; Search time 13.6667 Seconds (without alignments) 288.506 Million cell updates/sec Run on:

US-08-765-244-1 208 1 MLSNLRILLNKAALRKAHTS.....VRNFRYGKPVQSQLKPRDLC 41 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ripti	ornithine carbamoy		ornithine carbamoy	ornithine transcar	ornithine transcar	GTP binding conser	~			_	72	cyclin B5 - yeast	g	En/Spm-like transp	probable pilin, ty	proopiomelanocorti	corticotropin / li	WD-repeat protein	hypothetical prote	_	14	hypothetical prote	hypothetical prote	spoU family of rRN	hypothetical prote	Ē	hypothetical prote	щ	anthranilate synth
QI	OWRT	OWMS	OWHU	152779	A48421	F90409	B71413	S58250	F81900	G70233	B83922	S31290	B81708	152305	F75504	B45359	CTONPK	T50211	T23130	T32637	I40646	F91180	H86026	AD3351	T32702	AB0194	S	B69518	NNEC2
DB	<u>:</u> -	7	٦	7	7	7	(7	N	N	~	N	~	ď	N	N	N	-	N	N	N	C4	~	~	~	~	7	N	Н	ᆏ.
Length	354	354	354	41	350	351	1286	1468	138	260	383	435	185	306	314	240	258	206	1779	181	425	178	178	276	300	320	353	355	531
ry	. 9	69.5	0	m	~	7	9	9	9	2	S	S	S	4	4	4	24.5	4	4	'n	m	Э	'n	'n	3	3	3	3	m
SC	179	144	125	112	57	57	56	S	4	53.5	m		52.5	ä	ή.	51	51	51	S	49.5	ď	49	49	49	49	49	49	49	49
Result No.		7	m	4	Ŋ	Q	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

anthranilate synth hypothetical prote	anthranilate synth	probable sulfatase	invasin - Yersinia	Div protein [impor	cation-transportin	protein-tyrosine k	ribosomal protein	probable proteasom	proteasome endopep	hypothetical prote	hypothetical prote	subtilisin-like pr	hypothetical prote	cytochrome-c oxida
C90858 E85761	AE0653	F83354	A29646	A10802	877052	805582	T43306	A71033	B75181	B87613	S76749	T04186	T29621	111798
0 0	7	~	Н	~	N	-	N	N	C	N	C)	C)	7	7
531 531	531	538	986	333	945	1114	68	260	260	362	633	765	893	260
ب ب	φ	φ	ب	e.	m	m	-	-	-	-	-	!	Н.	ω.
23.6	23.	23.	23.	23.	23	23	23	23	23	23	23	23	23	22
4 9 0 0	49	49	4 9	48.5	48.5	48.5	48	48	48	48	48	48	48	47.5
		m	_	'n	'n	_	m	σ.	_	_	~	m		Ŋ

### ALIGNMENTS

RESULT 1 OWRT
ornithine carbamoyltransferase (EC 2.1.3.3) precursor - rat N;Alternate names: citrulline phosphorylase; ornithine transcarbamylase
C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Feb-1986 #secuence revision 28-Feb-1986 #text_change 11-Jun-1999
C; Accession: A00563; A28042; A23090; S02466; I52976; I67609; I53457
 Rifferstguent, M.; Mutra, S.; Mort, M.; Tattbaha, M.; Nagata, S.; Kaziro, Y. Byon Natl Anad Gof H. S. A. 81, 7410-7416, 1984
A, Title: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoy
 A.Reteremore number: A00563; MUID:85063800; PMID:8095244 A.Accession: A00563
 A, Molecule type: mRNA
 A;Residues: 1-354 <tak1> A:Cross-references: GR:K03040: NTD:G205873: PTDN:AAA41768.1: PID:G205874</tak1>
 ,
 A/ititle: Structure of the rat Conitthine carbamovitransierase gene, a Large, X Chiomos B.Pafaranca numbar. 202042. MITD:87317869: BWTD:3476935
A; Accession: A28042
A; Molecule type: DNA
A)CTOSS_TELEFENCES: GE:MIDS33; GE:JUJ290/, NID:G200864; LIUN:AAA41.009.1; FILD:G400000 D.VERSENCESTED BY THE PROPERTY OF THE P
Nucleic Acids Res. 13, 943-952, 1985
A; Title: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamyla
A. Reference number: A23090; MUID:85215524; PMID:3839075
A; ACCESSION: AZSUYU A: MOIDON! AZSUYU
A; Mediques: 1-38, P', 40-240, 'S', 242-354 <kra></kra>
A;Cross-references: GB:X01976
 R, Aoki, Y.; Sunaga, H.; Suzuki, K.T.
BLOCKER, J. 250, /35-/42, 1988 s.mitlo. s. asamina-binding mortain in rat liver identified as ornithing carbamov)tran
3
A; Accession: S02466
A; Molecule type: protein
CAUK>
s.a.; nuuson, F.G.; noogentaau,
A;Title: The primary structure of the imported mitochondrial protein, ornithine trans
 A; Reference number: 152976; MUID:85203360; PMID:3838931
 A;ACCESSION: 1224/0 b.ctatus translated from GR/FMRI/InRI
 A: Molecule type: mrnA
 A;Residues: 1-354 <res></res>
 A;Cross-references: GB:M11266; NID:9205871; PIDN:AAA41767.1; PID:9205872 B:Motttyre B : Graf I. Marcer I. Peterson G : Hudson P II: Hoodenraad, N.
 FDBS Lett. 177, 41-46, 1984
 A, Title: A highly basic N-terminal extension of the mitochondrial matrix enzyme ornit
A):BETEFENCE DUMDRET: 15349/; MULD:85051832; FMID:9548/14 A:BETEFENCE DUMDRET: 15746/9

~

us-08-765-244-1.rpr

```
With the carbamoy)transferse (EC 2.1.3.3) Precursor - human continue carbamoy)transferse (EC 2.1.3.3) Precursor - human continue carbamoy)transferse (EC 2.1.3.3) Precursor - human continue carbamoy) Miles (EC 2.1.3.4) Precursor - All 144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184144, 184114, 184144, 184114, 184144, 184114, 184144, 184114, 184144, 184114, 184144, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114, 184114,
                                          1;
                                          Gaps
                                       5
                                          Indels
                                                                                                                            1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                       .
.
                                       Mismatches
                                   .;
2
                                       Conservative
                                33;
                                Matches
                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                  g
                                                                                              ð
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-102 < RE2>
A; Cross references: EMBL:X01178; NID:956802; PIDN:CAA25618.1; PID:956803
A; Accession: 153457
A; Molecule type: mRNA
A; Residues: 143,'N',45-99,'R',101-102 < RE3>
A; Cross references: GB:K03041; NID:9205889; PIDN:AAA41771.1; PID:9205890
C; Genetics: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
C; Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
F; 1-32/Domain: transit peptide (mitcohondrino) #status predicted < NAT>
F; 40-342/Domain: aspartate/ornithine carbamoyltransferase #status predicted < NAT>
F; 40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: 155252; MUID:86224037; PMID:3011788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3
C; Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C; Superfamily: ornithine carbamoyltransferase; urea cycle
F; 1-32/Domain: transit peptide (mitochondrion) #status predicted <INP>
F; 33-335/Product: ornithine carbamoyltransferase #status predicted <AMT>
F; 40-342/Domain: aspartate/ornithine carbamoyltransferase #status predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-19,'LIMFDIF' <RES>
A;Cross-references: GB:M12716; NID:9200160; PIDN:AAA39864.1; PID:9554248
A;Note: the end of this sequence is near the boundary of the cloned region and may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ornithine carbamoyltransferase (EC 2.1.3.3) precursor - mouse
NiAlternate names: citrulline phosphorylase; ornithine transcarbamylase
CiSpecias: Mus musculus (house mouse)
CiSpecias: Mus musculus (house mouse)
CiSpecias: Mar-1993 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
CiAccession: A43609; S03407; I5252
Science 237, 415-417, 1987
Airlite: The molecular basis of the sparse fur mouse mutation.
Aireference number: A43609; MUID:87263407; PMID:3603027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mSNA
A:Cross-references: GB:MI7030; NID:g200162; PIDN:AAA39865.1; PID:g200163
B:Scherer, S.E.; Veres, G: Caskey, C.T.
Nucleic Acids Res. 16, 1593-1601, 1988
A:Title: The genetic structure of mouse ornithine transcarbamylase.
A:Reference number: S03407; MUD:88157717; PMID:2831503
A:Accession: S03407
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-194, R*, 196-335 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 179; DB 1; Length 354; Pred. No. 1.6e-17; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 144; DB 1;
Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: EMBL:X07092
R;Veres, G.; Craigen, W.J.; Caskey, C.T.
J. Biol. Chem. 261, 7588-7591, 1986
A;Title: The 5' flanking region of the o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.18;
92.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 92.9 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: OTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71413
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.;
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;
Avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdome erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; A;Title: Analysis of I.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Reference number: A71400; Muid: acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: I1286 <BEV>
A;Residues: I2284854
                                                                                                                                                                                                                                                                                                                                                                                                                                                   F99409
GTP binding conserved hypothetical protein SSO2385 [imported] - Sulfolobus solfatarios
GTP binding conserved hypothetical protein SSO2385 [imported] - Sulfolobus solfatarios
GTP binding conserved hypotheticals
GTP binding Sulfolobus solfatarios
GTP binding Sulfolobus Solfatarios
GTP binding Sulfolobus Solfatarios
GTP CONGY L; Allard, G.; Awayez, M.J.; C
GTP CONGY L; Allard, G.; Kozera, C.J.; Medina, M.; Peng, X.; Thi-Ngoc, H.P.; Redde arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A.Reference number: Applia Solfatarious complete genome.
A.Reference number: Applia
A.Recession: FP0409
A.Retus: preliminary
A.Molecule type: DNA
A.Recessides: 1-351 < KURN>

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross references: GB:AE006641; NID:913815687; PIDN:AAK42533.1; GSPDB:GN00155
C; Genetics:
A; Gene: SS02385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-directed DNA polymerase (EC 2.7.7.7) - yeast (Saccharomyces cerevisiae) N;Alternate names: DNA polymerase I; protein N2181; protein YNL102w C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ILLINKAA-----LRKAHTSMVRNFRY----GKPVQSQ------LKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 4COP9-4G3845
C;Superfamily: Arabidopsis thaliana hypothetical protein dl3525w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.9%; Score 56; DB 2; Length 1286; Best Local Similarity 35.3%; Pred. No. 19; Matches 12; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 351;
                                                           1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLKPRDL 40
                                                                                                                                                   |||| :|: :: | |:||| |:| :: | |:|| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.4%; Score 57; DB 2;
32.7%; Pred. No. 3.3;
tive 8; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein d13525w - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress) A;Variety; columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 32.7%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
S58250
                                                           ŏ
                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ornithine transcarbamylase - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A44421
R;Helbing, C; Gergely, G; Atkinson, B.G.
Bev. Genet. 13, 289-310, 1995
A;Tille: Sequential up-regulation of thyroid hormone beta receptor, ornithine transcarbd thyroid hormone-induced metamorphosis.
A;Reference number: A48421; MUID:93177976; PMID:1291156
A;Accession: A48421
A;Accession: A48421
A;Accession: A48421
A;Molecule type: nucleic acid
A;Residues: 1-350 AEIL
A;Coss-references: GB:M95193; NID:9213683; PIDN:AAA49528.1; PID:9213684
A;Coss-references: GB:M95193; NID:9213683; PIDN:AAA49528.1; PID:9213684
A;Coss-references: GB:M95193; NID:9213684
A;Coss-references: GB:M95193; NID:9213683; PIDN:AAA49528.1; PID:9213684
A;NOte: Sequence extracted from NCBI backbone (NCBIN:126155)
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C;Keywords: mitochondrion
F;36-338/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
e synthesis of UMP.

C.Gometics:
A.Genetics:
A.Genetics:
A.Genetics:
A.Genetics:
C.Genetics:
C.Genetics:
A.Genetics:
A.Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbamoyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οį
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ornithine transcarbamylase peptide - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 25-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999
C;Accession: 152779
R;Horwich, A.L.; Kalousek, F.; Fenton, W.A.; Pollock, R.A.; Rosenberg, L.E.
R;Horwich, 451-459, 1986
A;Title: Targeting of pre-ornithine transcarbamylase to mitochondria: Definition A;Reference number: 152779; MUID:86106223; PMID:3943133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: GB:MI2583; NID:g205887; PIDN:AAA41770.1; PID:g205888
C)Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 27.4%; Score 57; DB 2; Length 350; Best Local Similarity 40.0%; Pred. No. 3.3; Matches 16; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.1%; Score 125; DB 1; Length 35
Best Local Similarity 66.7%; Pred. No. 7.3e-10;
Matches 28; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.8%; Score 112; DB 2; Length 41 Best Local Similarity 61.1%; Pred. No. 4.7e-09; Matches 22; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A)Residues: 1-41 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

ä

ó

Fri

```
hypothetical protein BBG23 - Lyme disease spirochete plasmid G/lp28-2
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-oct-1999
C;Accession: G70233
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W; Soon, D.; Peterson, J.; Kerlayde, A.R.; Queokenbush, J.; Salzberg, S.; Hanson, M.; V; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, S80-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70233
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type DRA
A;References: GB:AE000786; NID:92690008; PIDN:AAC66071.1; PID:92690028; TIGR:BE
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid
           C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: F81900
C;Accession: F81900
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc
N; Hollroyd, S; J; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
N; Holler Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 2249;
A;Recence number: A81775; MUD:20222556; PMID:10761919
A;Accession: F81900
A;Status: preliminary
A;Accession: F81900
A;Status: Draiminary
A;Residues: 1-138 CPAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB84568.1; PID:G737
A;Cross-references: Serogroup A, strain 22491
A;Generics:
A;Generics:
A;Generics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <GNA
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05897;1; GSPDB:C
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID: 92690008; PIDN: AAC66071.1; PID: 92690028; TIGR: BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Short-chain-specific acyl-CoA dehydrogenase BH2178 [imported] - Bacillus halodurans c;Species: Bacillus halodurans c;Species: Bacillus halodurans c;Species: Bacillus halodurans c;Dacession: B39322 BC-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 R.Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000 A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A93650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QLKPRDLC
                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                              Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.7%; Score 53.5; DB 2; 21.8%; Pred. No. 7.4; ive 14; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 RILLNKAALRKAHTSMVRNFRY-GKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 RYLLMRRLSETMHTAVKLNFRYAGRPKWLGLKYRD 60
                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RILLNKAALRK-----AHTSMVRNFRYGKPVQS-
                                                                                                                                                                                                                                                                                                                                                                              Score 54.5; D
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.2%;
Best Local Similarity 42.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.7%
Best Local Similarity 21.8%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
protein NMA1316 [imported] - Neisseria meningitidis (strain 22491 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPILICES IQTIMNPKENKQEIVSITLSAYRNISLDSPIPENIKPDDLC 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSNLRILL------NKAALRKAHTSMVRNFRYGKPVQSQLKPRDLC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: SGD:S0005046; MIPS:YNL102w
A;Map position: 14L
C;Superfamily: herpesvirus DNA-directed DNA polymerase
C;Keywords: nucleoridyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; DE
Pred. No. 26;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 29.4%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F81900
hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ДQ
```

ទីទី៣

æ

5,

δλ g

```
En/Spm-like transposon protein [imported] - Arabidopsis thaliana
NyAlternate names: protodermal factor 1
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 16-Feb-2001
C.Accession: T52305; H84858
R.Abe, M.; Takhasahi, T.; Komeda, Y.
Plant Cell Physiol. 40, 571-580, 1999
A.Title: Cloning and characterization of an Ll layer-specific gene in Arabidopsis this A; Reference number: 226029; MUID: 99412619; PMID: 10483121
A.Accession: T52305
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-306 (AABE)
A.Cross-references: EMBL:AF141375; PIDN:AAD33868.1
A.Experimental source: cultivar Columbia, meristem Ll layer
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentco, M.I.; Town, C.D.; Fujli, C.J.
M.; Koo, H.; Woffat, K.S.; Gronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
A.Accession: H84858
A.Accession: H84858
A.Accession: H84858
A.Accession: H84858
A.Accession: H84858
A.Accession: H84858
A.Accession: B4420; MUID:20083487; PMID:10617197
A.Accession: B4420840
A.Accession: PDFI, At4942840
    A;Molecule type: DNA
A;Residues: 1-185 <TET>
A;Cross-references: GB:AE002306; GB:AE002160; NID:97190428; PIDN:AAF39255.1; PID:9719
C;Genetics:
A;Gene: TC0398
C;Superfamily: translation elongation factor EF-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable pilin, type IV - Deinococcus radiodurans (strain R1)
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Dainococcus radiodurans
Cispecies: Dainococcus radiodurans
Cispecies: Dainoccus radiodurans
Cispecies: Dainoccus Cispecies: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 306;
                                                                                                                                                                                                                                                                                                                                                                          Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                           Query Match

25.2%; Score 52.5; DB 2;
Best Local Similarity 42.4%; Pred. No. 7.1;
Matches 14; Conservative 9; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 KAALRKAHTSMV--RNFRYGKPV-QSQLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51.5; DE Pred. No. 17; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 NKAATKQAHTFKLAN-----EGRLKPR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NKAALRKAHTSMVRNFRYGKPVQSQLKPR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
$31290
cyclin B5 - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein P9642.8; protein rpR120c
C;Species: Saccharomyces cerevisiae
C;Species: Cas. Cross, F.R.
Comes Dev. G, 1659-1706, 1993
A;Title: CLB5: a novel B cyclin from budding yeast with a role in S phase.
A;Reference number: S31290; MUID:92387544; PMID:1387626
A;Molecule type: DNA
A;Residues: 1-435 <EPS>
A;Title: CLB5 and CLB6, a new pair of B cyclins involved in DNA replication in Saccharom A;Reference number: S36228; MUID:93307652; PMID:8319908
A;Schwob. E; Nasmyth, K
A;Reference number: S36228; MUID:93307652; PMID:8319908
A;Reference number: S36228
A;Schwob: Castle CLB5
A;Recomber: CLB5
A;Recomber: S36228
A;Reference number: S36228
A;Reference number: S3628
A;R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-435 <JOH>
A;Cross-references: EMBL:U40828; NID:91066467; PIDN:AAB68061.1; PID:91066475; MIPS:YPR12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Chlamydia muridarum, Chlamydia trachomatis MoPn (Species: Chlamydia muridarum, Chlamydia trachomatis MoPn (Species: Chlamydia muridarum, Chlamydia trachomatis MoPn (Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000 (SAccession: B81708 F; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255; PMID:10684935 A; Status: preliminary
                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                        Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 2; Length 435;
Pred. No. 15;
4; Mismatches 11; Indels
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Johnson, D. Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of S. cerevisiae cosmid 9642.
A;Reference number: S69014
A;Recession: S69013
                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                   2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                              Score 53.5; D
Pred. No. 11;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SNLRILLNKAALRKAHTSMVRNFRYGKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 SNLKILQNKRALSKNDSSKQQVQDSKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.5%;
                                                                                                                     Query Match 25.7%;
Best Local Similarity 42.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Cross-references: SGD:S0006324
A Map Position: 16R
C; Superfamily: cyclin
C; Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 46.4 nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SGD:CLB5; CLB5
C;Genetics:
A;Gene: BH2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
```

η Ω Ν

ij

δ

```
A;Residues: 1-314 <NHI>
A;Cross-references: GB:AE001913; GB:AE000513; NID:g6458240; PIDN:AAF10127.1; PID:g645824
A;Experimental source: strain R1
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Amp position: 1
                                                                                                                                                                                                            2;
                                                                                                                                                               Query Match 24.8%; Score 51.5; DB 2; Length 314; Best Local Similarity 43.8%; Pred. No. 18; Matches 14; Conservative 4; Mismatches 9; Indels 5; Gaps
                                                                                                                                                                                                                                                  Search completed: July 24, 2003, 22:08:06 Job time : 16.6667 secs
                                                                                                                                                                                                                                                         · 03
                                                                                                                                                                                                                                                                                               g
```

```
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

July 24, 2003, 21:59:48; Search time 7:32143 Seconds (without alignments) 263.350 Million cell updates/sec

US-08-765-244-1 208 1 MLSNIRILLINKAALRKAHTS.....VRNFRYGKPVQSQLKPRDLC 41 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	P00481 rattus norv	snw snw	homod	rana	sacch						0								homo sapi		P59289 schizosacch			buchnera		ovis arie	Q9zcx7 rickettsia		P05733 schizosacch	Q8u016 pyrococcus	535	_	4
SOUTHWANTES	QI	OTC_RAT			OIC		RR2_						POF									R37A			SYR_E	X37	NRMI		CYGI	R37B_	PSM		MEUI	
	Length DB	354 1																	985	739		88												
*	Match	86	69.2	0	^	9	9	ហ	Ω	Ŋ	4	₹"	4	4	4	4	'n	ص	23.6	m.	٠ ش	23.1	m.	m	m	22.8	'n.	· ·	ni.		ς.	~	~	٠.
	Score	_	144	CA.	n	55.5	54	53	ഗ	52.5	51	51	51	20	20	20	49	49	49	4	48.5	48	80	48	7	٠,	47.5	٠.	۲.		47		47	47
Result	NON	П	7	m	4	ഗ	φ	7	00	on ;	10	H .	15	e i	14	12	9 1	17	18	19	20	21	22	23	7.7	25	97	17	28	52	90	31	3.5	ဗ

09y7j8 schizosacch P57110 mus musculu 07585 home sapien P43726 haemophilus 097tx6 sulfolobus P4970 home sapien 024733 thermococcu 09pj8 campylobact 08pj8 campylobact 08pg7 versinia pe P37126 xanthomonas
YGLI_SCHPO ATSB_MOUSE MOUSE MOUSE MOUST_MOUNAN NIS_HOMAN MIS_HOMAN MSRA_SULSO MSRA_THEKI FWT_CAMJE TRPD_YERPE CGLH_XANMA
<b>нанананана</b>
883 1050 1050 1442 1473 1905 1905 1905 1905 1905 1905 1905 1905
444 600 444 • • • • 44444 7 • • • • • • • • • • • • • • • • • • •
888888884444 45867886017845

## ALIGNMENTS

RESULT OTC_RA	NESULT 1 OTC_RAT STANDARD: DRT: 354 AA
AC.	P00481; Q63407;
Į į	21-JUL-1986 (Rel. 01, Created)
i	21-JUL-1980 (Kel. Ul, Last Sequence update) 16-00m-2001 (Del 10 lest ennotation undate)
DE	or or the carbamovitransferase, mitochedus necessary (EC 2 1 3 3)
DE	
S G	OTC
3 S	kattus norvegicus (kat). Eukarvota: Metazoa: Chordata: Craniata: Vartebrata: Enteleostomi:
8	
XO.	
R.	[1]
RP 4	SEQUENCE FROM N.A. Meditne-brokson. D.:bw.d-forese.
R.	Takiquchi M. Miura S. Mori M. Tatibana M. Nadata S. Kaziro V
RT	
RT	
고 2	Proc. Natl. Acad. Sci. U.S.A. 81:7412-7416(1984).
Z C	( Z)
7 A	SHEADENCE FROM N.A.
×	MEDITNE=87317609
RA	Tekidischi M. Mirakami F. Mirra S. Mori M.
RT	"Structure of the rat ornithine carbanovirus."
RT	dene with an atypical promoter.":
RL	
RN	[3]
RP	SEQUENCE FROM N.A.
RX	
RA	Kraus J.P., Hodges P.E., Williamson C.L., Horwich A.L., Kalousek F.,
KA i	
¥ £	ornithine
בל 12	Transcarbamylase: comparison of rat and human leader sequences and
120	Conservation Or Carcarfuls. /
R.	14.
RР	SEQUENCE FROM N.A.
RX	MEDLINE=85203360; PubMed=3838931;
RA	McIntyre P., Graf L., Mercer J.F.B., Wake S.A., Hudson P.J.,
RA	Hoogenraad N.;
RT	iry structure of the imported mitochondrial pr
R.	ornithine transcarbamylase from rat liver: mRNA levels during
K	ontogeny,";
Z 2	DNA 4:14/-156(1985).
2 2	101 SECHTENCE OF 33-56. 203-302. 307-317 BND 321-220
R C	1
RX	MEDLINE-88268748; PubMed-3390141;
R.	
RI	"A cadmium-binding protein in rat liver identified as ornithine
7 H	Carbamoyttransterase.; b:oro.nortransterase.;
<u> </u>	DICCHEM. J. 201135-144(1988). -1- CREWILYWIT ACTIVITY. Carbancel phosphate + I-ornithine = phosphate
}	oyi phosphace + m-offitching =

```
Veres G., Craigen W.J., Caskey C.T.;
"The 5' flanking region of the ornithine transcarbamylase gene
contains DNA sequences regulating tissue-specific expression.";
J. Biol. Chem. 261:7588-7591(1986)
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                        SEQUENCE FROM N.A.
MEDIINE-8815717; Pubmed-2831503;
Scherer S.E., Veres G., Caskey C.T.;
"The genetic structure of mouse crnithine transcarbamylase.";
Nucleic Acids Res. 16:1593-1601(1988).
             MEDLINE-87263407; PubMed-3603027; Veres G., Glbbs R.A., Scherer S.E., Caskey C.T.; "The molecular basis of the sparse fur mouse mutation."; Science 237:415-417(1987).
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-26 FROM N.A.
STRAIN-C57BL/6J;
MEDLINE-86224037; PubMed-3011788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
354
263
303
1117
195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97448; Otc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transit peptide.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                REPRESENTATION OF THE PRESENTATION OF THE PRES
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTGase) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
+ L-citrulline.

PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.

SUBUNIT: Homotriner.

SUBCELLULAR LOCATION: Mitochondrial matrix.

SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0100; AOTCASE.
TIGRAMS; TIGRO0658; OTCAL_CATA_LT; 1.
PROSTIE; PS00099; CARBAMOTIRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORNITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
G -> P (IN REF. 3; AAA41772).
G -> S (IN REF. 3).
156B511AF7063F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 179; DB 1; Length 354;
Pred. No. 2.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPRO06130, Asp/orn_Cotranf.
InterPro: IPRO02292; Orn_carbtransf.
InterPro: IPRO06131, OrCace_O.
InterPro: IPRO06131, OrCace_P.
Pfan; PPO0185; OrCace; I.
Pfan; PPO0185; OrCace; I.
                                                                                                                                                                                                                                                                                                                                                           EMBL, K03040; AAA41768.1; EMBL, M16924; AAA41769.1; EMBL, M16924; AAA41769.1; EMBL, M16926; AAA41769.1; JOINED. EMBL, M16926; AAA41769.1; JOINED. EMBL, M16926; AAA41769.1; JOINED. EMBL, M16929; AAA41769.1; JOINED. EMBL, M16930; AAA41769.1; JOINED. EMBL, K01976; CAA26007.1; EMBL, K01976; CAA26007.1; EMBL, K01976; CAA26007.1; EMBL, M1266; AAA41772.1; EMBL, M1266; AAA41767.1; FISSP; P00480; JOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39886 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sh 86.1%;
1 Similarity 92.9%;
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
263
263
303
39
241
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fransit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTC_MOUSE
P11725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
OTC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
+ L-citrulline.
-- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
-- SUBGELLULAR: Homotrimer.
-- SUBCELLULAR LOCATION: Mitochondrial matrix.
-- DECREASE: SPRRSE FUR (SPF) MOUSE HAVE AN OTC WITH AN OVERALL DECREASE IN ACTIVITY, AND ALTERED SUBSTRATE AFFINITY.
-- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00100; AOTCASE.
TIGREAMs; TIGR00658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYITRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORNITHINE CARBAMOYLIRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
H -> N (IN SPARSE FUR MOUSE).
G -> R (IN REF. 2).
W; 33BBE5DIE88AA196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.2%; Score 144; DB 1; Length 354; llarity 78.6%; Pred. No. 2.6e-13; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006130; Asp/orn_cotranf.
InterPro; IPR002292; Orn_carbtransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
Pfam; PF00185; OTCace; I.
Pfam; PF02729; OTCace_N; I.
```

δŏ

m

```
MEDLINE=95353279; PubMed=7627182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum.
 MEDLINE-20274073; PubMed-10813810;
Shi D., Morizono H., Aoyagi M., Tuchman M., Allewell N.M.;
"Crystal structure of human ornithine transcarbamylase complexed with
carbamoyl phosphate and L-norvaline at 1.9 A resolution.";
Proteins 39:271-277(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutations and polymorphisms in the human ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                  Horwich A.L., Fenton W.A., Williams K.R., Kalousek F., Kraus J.P., Doolittle R.F., Konigsberg W., Rosenberg L.E.; Structure and expression of a complementary DNA for the nuclear coded precursor of human mitochondrial ornithine transcarbamylase.";
                                                                                                                                          precursor (EC 2.1.3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
;;
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcarbamoylase complexed with N-phosphonacetyl.L-ornithine. Catalytic mechanism and correlation with inherited deficiency."; J. Biol. Chem. 273:34247-34254(1998).
                                                                                                                                                                                                                                           TISSUE-Liver;
MEDINE-88127905; PubMed=2836378;
MEDINE-881270905; PubMed=2836378;
Hata A., Tsuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda "Structure of the human ornithine transcarbamylase gene.";
J. Biochem. 103:302-308(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-87057134; PubMed-3782067;
Hata A., Tsuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda "Isolation and characterization of the human crnithine transcarbamylase gene: structure of the 5'-end region."; J. Biochem. 100:717-725(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE=99069419; PubMed=9852088;
Shi D., Morizono H., Ha Y., Aoyagi M., Tuchman M., Allewell N.M.
"1.85-A resolution crystal structure of human ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85270440; PubMed=3895227;
HOTWICH A.L., Kalousek F., Rosenberg L.E.;
"Arginine in the leader peptide is required for both import approteolytic cleaved a mitochondrial precursor.";
Proc. Natl. Acad. Sci. U.S.A. 82:4930-4933(1985).
 40
                       42
            MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL
                                                                                                   11-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
07-Case) (Ornithine carbamcyltransferase, mitochondrial
                                                                                354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                        MEDLINE=84196410; PubMed=6372096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93372868; PubMed-8364586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Mutat. 2:174-178(1993)
                                                                                                                                                                                                                                                                                                                                                                                                 Science 224:1068-1074(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-36 FROM N.A.
                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVIEW ON VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [8]
REVIEW ON VARIANTS.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Puchman M.;
                                                                                OTC_HUMAN
                                                                                           P00480;
                                                         RESULT
ö
                     g
```

```
Glibert-Dussardier B., Radier D., Strautnieks S., Seques B., Bonnefont J.-P., Munnich A.; Bonnefont J.-P., Munnich A.; A novel arginine (245) to glutamine change in exon 8 of the ornithine carbamoyl transferase gene in two unrelated children presenting with late onset deficiency and showing the same enzymatic pattern.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grompe M., Muzny D.M., Caskey C.T.; "Scanning detection of mutations in human ornithine transcarbamoylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatal hyperammonemia resulting from a C-to-T mutation at a MspI site of the ornithine transcarbamylase gene."; lum. Genet. 88:153-156(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   þλ
                                         human ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS OTCD GLU-79; THR-94; PHE-304 AND ASP-345.
MEDLINE-93126062; PubMed-1480464;
Tuchman M., Holzknecht R.A., Gueron A.B., Berry S.A., Tsai M.Y.;
"Six new mutations in the ornithine transcarbamylase gene detected single-strand conformational polymorphism.";
Pediatr. Res. 32:600-604(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .D.;
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT OTCD GLN-141.
MEDLINE-89008892; PubMed-3170748;
Maddalena A., Spence J.E., O'Brien W.E., Nussbaum R.L.;
"Characterization of point mutations in the same arginine codon three unrelated patients with ornithine transcarbamylase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seguencing
                                                                                                                                                                                  REVIEW ON VARIANTS, AND 3D-STRUCTURE MODELING.
MEDLINE-96091868; PubMed-8544185;
Tuchman M., Morizono H., Reish O., Yuan X., Allewell N.M.;
The molecular basis of ornithine transcarbamylase deficiency:
modelling the human enzyme and the effects of mutations.";
J. Med. Genet. 32:680-688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91118929; PubMed=1671317;
Grompe M., Caskey C.T., Fenwick R.G. Jr.;
"Improved molecular diagnostics for ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90269805; PubMed-2347583; Finkelstein J.E., Francomano C.A., Brusilow S.W., Traystman M. Finkelstein J.E., Francomano C.A., Brusilow S.W., Traystman M. Tase of denaturing gradient gel electrophoresis for detection mutation and prospective diagnosis in late onset ornithine transcarbamylase deficiency."; Genomics 7:167-172(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS OTCD GLN-26; PRO-45 AND GLU-216, AND VARIANT ARG-46 MEDLINE-89345570; PubMed-2474822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92098086; PubMed-1721894;
Hertzen D., Pelet A., Feldman D., Rabier D., Berthelot J.,
Munnich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 269-289 FROM N.A., AND VARIANT OTCD GLN-277.
MEDLINE=94362689; PubMed-8081373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isai M.Y., Holzknecht R.A., Tuchman M.;
"Single-strand conformational polymorphism and direct
applied to carrier testing in families with ornithine
transcarbamylase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS OTCD GLN-92 AND LEU-320, AND VARIANT PRO-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by chemical mismatch cleavage.";
Proc. Natl. Acad. Sci. U.S.A. 86:5888-5892(1989)
Tuchman M., Plante R.J.;
"Mutations and polymorphisms in the
gene: mutation update addendum.";
Hum. Mutat. 5:293-295(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am. J. Hum. Genet. 48:212-222(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Invest. 82:1353-1358(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1721894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93273296; PubMed=8099056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Genet. 3:831-832(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT OTCD TRP-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT OTCD LEU-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT OTCD PRO-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deficiency
```

precursor (EC 2.1.3.3)

350 AA

STANDARD;

ornithine

```
Rep. Fac. Sci. Shizouka Univ. 29:45-54(1995).
-!- FUNCTION: OTC IS NECESSARY FOR THE TADPOLES TRANSITION FROM AN
AMMONOTELIC, AQUATIC LARVA TO A UREOTELIC, TERRESTRIAL ADULT.
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                      (OTCase) (Ornithine transcarbamylase).
Rana catesbelana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibla; Batracchia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                    Helbing C., Gergely G., Atkinson B.G.; "Sequential up-regulation of thyroid hormone beta receptor, ornith transcarbamylase, and carbbamyl phosphate synthetase mRNAs in the liver of Rana catesbelana tadpoles during spontaneous and thyroid hormone-induced metamorphosis."; Dev. Genet. 13:289-301(1992).
                                                                                                                                                                                                                                                                                                                                                                                     Iwase K., Yamauchi K., Ishikawa K.;
"Molecular cloning of bullfrog (Rana catesbeiana) ornithine
transcarbamylase and induction of its mRNA during spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       + L-citrulline.
--- PATHARY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
--- SUBBUNIT: HOMOTIMER.
--- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
01 Lithine carbamoyltransferase, mitochondrial
                                                                                                                                                                                                                                     MEDLINE-93177976; PubMed-1291156;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          metamorphosis.";
       Tuchman M., Plante R.J., Giguere Y., Lemieux B., "The contithine transcarbamylase gene: new 'private' mutations in four patients and study of a polymorphism."; Hum. Mutat. 3:318-320(1994)
                                                                                                                                                                                                            Four newly identified ornithine transcarbamylase (OTC) mutations (D1266, R129H, I172M and W332X) in Japanese male patients with early-onset OTC deficiency.";
                                                                                                                                                                                                                                                                                                                                                                Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.; "Seven new mutations in the human ornithine transcarbamylase gene."; Hum. Mutat. 4:57-60(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A splicing mutation, a nonsense mutation (Y167X) and two missense mutations (I1597 and A2089) in Spanish patients with ornithine transcarbamylase deficiency."; Hum. Genet. 96:549-551(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS OTCD MET-125; ARG-188; VAL-209 AND LEU-302.
MEDLINE-96400964; PubMed-8807340;
Gilbert-bussardier B., Segues B., Rozet J.-M., Rabier D., Calvas P.
de Lumley L., Bonnefond J.-P., Munnich A.;
"Partial duplication [dup. TGAC (178)] and novel point mutations
(T125M, G188R, A209V, and H302L) of the ornithine transcarbamylase
gene in congenital hyperammonemia.";
                                                                                                                                                            MEDLINE-94362715; PubMed-8081398; Matsuura T., Hoshide R., Kiwaki K., Komaki S., Koike E., Endo F., Oyanagi K., Suzuki Y., Kato I., Ishikawa K., Yoda H., Kamitani S. Sakaki Y., Matsuda I.;
                                                                                                                                                                                                                                                                                                                                                                                                                              VARÍANTS OTCD THR-159 AND VAL-209.
MEDLINE-96070988; PubMed-8530002;
Garcia-Perez M.A., Sanjurjo P., Briones P., Garcia-Munoz M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS OTCD HIS-40, ASN-88; TYR-202 AND ASN-263.
Guardamagna O., Gatti E., Parini R., Plante R.J., Tuchman M.;
"Genotype-phenotype correlations in ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                             VARIANTS OTCD HIS-40; HIS-129; ARG-195; THR-225; GLN-277 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96086561; PubMed=7474905; Zimmer K.P., Matsuura T., Colombo J.-P., Koch H.G., Ullrich Deufel T., Harms E., Matsuda I.; A novel point mutation at codon 269 of the ornithine transcarbamylase (OTC) gene causing neonatal onset of OTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS OTCD ASN-88; CYS-176; ALA-220; TYR-302 AND LYS-343.
MEDLINE-97114289; PubMed-8956038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 125; DB 1; Length 354; Pred. No. 1.5e-10;
                                   LEU-182 AND CYS-203.
                                                                                                                                                  VARIANTS OTCD GLY-126; HIS-129 AND MET-172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inherit. Metab. Dis. 18:356-357(1995).
                                 VARIANTS OTCD LEU-117; LEU-182 AN:
MEDLINE=94290509; Pubmed=8019569;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=95038770; PubMed=7951259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzyme Protein 49:191-191(1996).
 Hum. Genet. 91:321-325(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.1%;
66.7%;
                                                                                                                                                                                                                                                                                 Hum. Mutat. 3:402-406(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutat. 8:74-76(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.7
nes 28; Conservative
                                                                                                                                                                                                                                                                                                                                  DEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
-i-TISSUE SPECIFICITY: LIVER.
-i- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
-i- INDUCTION: By thyroid hormone.
-i- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00100; AOTCASE.
TIGRPAMS; TIGR00658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION (BY SIMILARITY).
ORNITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
; E1ES98355F03C13E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 1; Length 350;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                             PIR; A48421; A48421.
HSSP; P00480; 10TH.
InterPro; IPR006130; Asp/orn_cotranf.
InterPro; IPR002292; Orn_carbtransf.
InterPro; IPR006131; OfCace_0.
InterPro; IPR006132; OfCace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39636 MW;
                                                                                                                                                                                                                                                                                                   EMBL; M95193; AAA49528.1; -. EMBL; D38304; BAA22775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00185; OTCace, 1. Pfam; PF02729; OTCace_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350
259
299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
299
350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
```

Gaps

5

9; Indels

3; Mismatches

Best Loc Matches

ð g RESULT 4 OTC\_RANCA

ð

```
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                    DARAMARA DORRANA DORRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1-FUNCTION: Polymerase alpha in a complex with DNA primase is a replicative polymerase. Has a role in promoting telomere replication during interaction with CDC13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with CDC13.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULANEOUS: In eukaryotes there are five DNA polymerases:
ALSCELLANEOUS: In eukaryotes there are five DNA polymerases:
ALDPA, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase alpha catalytic subunit (EC 2.7.7.7) (DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND MUTAGENESIS OF GLY-493.
MEDLINE-88234507, PubMed-3-287376,
Pizzagalli A., Valsasnini P., Plevani P., Lucchini G.;
"DNA polymerase I gene of Saccharomyces cerevisiae: nucleotide sequence, mapping of a temperature-sensitive mutation, and protein homology with other DNA polymerases.",
Proc. Natl. Acad. Sci. U.S.A. 85:3772-3776(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saiz J.E., Buitrago M.J., Soler A., del Rey F., Revuelta J.L.; "The sequence of a 21.3 kb DNA fragment from the left arm of yeast chromosome XIV reveals LEU4, MET4, POL1, RAS2, and six new open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=20357110; PubMed=10898792;
Q1 H., Zakian V.A.
"The Saccharomyces telomere-binding protein Cdc13p interacts with
the catalytic subunit of DNA polymerase alpha and the telomerase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mountain H.A., Bystroem A.S., Korch C.;
"The general amino acid control regulates MET4, which encodes a methiconine-pathway specific transcriptional activator of Saccharomyces cerevisiae.";
                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLKPRDL
                                                                                                                                                                                                                                                                                                                                                1468 AA
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POL1 OR CDC17 OR YNL102W OR N2181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c / FY1679;
MEDLINE=96267765; PubMed=8701612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288c;
MEDLINE=93188702; PubMed=8446029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol, 7:215-228(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated estl protein.";
Genes Dev. 14:1777-1788(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ceast 12:403-409(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, AND SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DNA)(N)
                                                                                                                                                                                                                                                                                                                                      DPOA_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reading
                                                                                                                                                                                                                                                                                        DPOA_YEAST
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 493 G -> R (IN TEMPERATURE SENSITIVE MUTANT).
759 760 MI -> IV (IN REF. 1).
1468 AA; 166808 MW; 50C9032DBE95B5AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 MPNLRCLSLSIQTLMNPKENKQEIVSITLSAYRNISLDSPIPENIKPDDLC 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LSNLRILL------NKAALRKAHTSMVRNFRYGKPVQSQLKPRDLC 41
EMBL; J03268; AAA34888.1; -

EMBL; Z50161; CAA90524.1; -

EMBL; Z12168; CAA9598.1; -

EMBL; Z12168; CAA969.1; -

EMBL; Z12168.2; CAA969.1; -

EMBL; Z12168.2; CAA969.1; -

EMBL; Z12168.2; CAA969.1; -

EMBL; Z12168.2; CAA969.2; -

EMBL; Z1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.7%; Score 55.5; DB 1; Length 1468; 29.4%; Pred. No. 9.1; Live 4; Mismatches 21; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30s ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001865; Ribosomal_S2. Interpro; IPR005706; S2_bact_org. Pfam: PF00318; Ribosomal_S2; 1. PRINTS; PR00395; RIBOSOMALGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO1011; rpsB_bact; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP002983; BAB33197.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lotus japonicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RR2_LOTJA
Q9BBS6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
```

ί;

us-08-765-244-1.rsp

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCIDENCE FROW N.A.

SUCH SIZES FROW N.A.

SUBCIDENCE FROW N.A.

BUSSEY H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Burajo R., Barrall B.G., Barcock K., Benes V., Bussey H., Storms R.K., Aparicio A., Barrall B.G., Dadocok K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Churcher C.M., Coster F., Davis R.K., Davis R.W., Dietrich F.S., Delius H., Dibaolo T., Dubois E., Duesterhoeft A., Dietrich F.S., Delius H., Dibaolo T., Dubois E., Duesterhoeft A., Bull J., Hebling U., Heumann K., Hilbert H., Hillier L., Annicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Annicke-Smith S., Mowes H.-W., Mirtipati S., Mosetl D., Anarathe R., Mewes H.-W., Mirtipati S., Mosetl D., Anarathe R., Newson H.-W., Mirtipati S., Mosetl D., Annicke-Smith B., Schramm S., Schroeder M., Schafer M., Schreiß B., Schramm S., Schroeder M., Schreiß B., Schramm S., Schroeder M., Schreiß B., Schramm S., Schroeder M., Schroeder M., Tettelin H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., And Dietride sequence of Saccharomyces cerevisiae chromosome.XVI.", Nature 387:103-105(1997).
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BF264-15D;
MEDLINE=92387544; PubMed=1387626;
Epstein C.B., Cross F.R.;
"CLBS: a novel B cyclin from budding yeast with a role in S phase.";
Genes Dev. 6:1695-1706(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AB320;
MEDLINE=93307652; PubMed=8319908;
Schwob E., Nasmyth K.;
"CLB5 and CLB6, a new pair of B cyclins involved in DNA replication in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1- FUNCTION: REQUIRED FOR EFFICIENT PROGRESSION THROUGH S PHASE AND POSSIBLY FOR THE NORMAL PROGRESSION THROUGH MEIOSIS. INTERACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-94074543; PubMed-8253070;
Kuehne C., Linder P.;
"A new pair of B-type cyclins from Saccharomyces cerevisiae that function early in the cell cycle.";
EMBO J. 12:3437-3447(1993).
                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-phase entry cyclin 5.
CLB5 OR YPR120C OR P9642. 8.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                ;
                                                                                 Length 236;
                                                                                                              Indels
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
Ribosomal proctein; Chloroplast.
SEQUENCE 236 AA; 26982 MW; CE9E238572325586 CRC64;
                                                                              26.0%; Score 54; DB 1; 38.5%; Pred. No. 1.9; ive 10; Mismatches
                                                                                                                                                                                                                                                       435 AA
                                                                                                                                                             211 IASIRLILNKLVFAICEGHSSYIRNF 236
                                                                                                                                          2 LSNLRILLNKA--ALRKAHTSMVRNF 25
                                                                      Query Match
Best Local Similarity 38.5%
Matches 10; Conservative
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N. A.
                                                                                                                                                                                                                                                    CGS5_YEAST
P30283;
                                                                                                                                                                                                                                      CGS5_YEAST
                                                                                                                                                                                                                       RESULT
   S KW DR
                                                                                                                                          ò
                                                                                                                                                                     g
                                                                                                                                                                                                                                                                    CCHE BARARARARARARARARARARARE BARARARARARARARARARARARARAROOO OO BEBAAA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO ATCC 35395 / DSW 2834;

MEDLINE-21929760; PubMed-11932238;

MEDLINE-21929760; PubMed-11932238;

A alagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Strange-Thomann N., Dearellano K., Johnson R., Linton L., McEwan P., McKernan K., Talanas J., Tirrell A., Yew W., Linton L., McEwan P., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kustroki J. R., K., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., McTchlett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., McTchlett W., Strens B.;

"The genome of Methanosarcha acetivorans reveals extensive metabolic General May Prince T. M., Shandaria, McTalay M., Shirton B., Gondon Res. J2:53-544(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: Function in general translation initiation by promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                         DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED JUST BEFORE CELL CYCLE
                                             START.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                  QBTQL5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Probable translation initiation factor IF-2.
INTR OR MAIS25
Methanosarcina acetivorans.
Archaea, Euryarchaeota, Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinales; Methanosarcinales;
NCBI_TAXID-2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.5%; Score 53; DB 1; Length 435; 46.4%; Pred. No. 5.4; ive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell cycle; Cell division; Multigene family.
E 435 AA; 50431 MW; 5AD67EB841BA5759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SNLRILLNKAALRKAHTSMVRNFRYGKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 SNLKILQNKRALSKNDSSSKQQVQDSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                EMBL, M91209, AAA34503.1; -. EMBL, X70435; CAA49893.1; -. EMBL, 140828; AAB680611.1; -. PIR; S31290; S31290. SGD; S0006324; CLBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
WITH CDC28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IF2P_METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IF2P_METAC
```

```
RESULT 10
COLI_ONCKE
       à
                                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish-sih.nh/annonnon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ñ
                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000)

Nucleic Acids Res. 28:1397-1406(2000)

TRANSLATION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MoPD / Nigg;
MEDLINE-20150255; Pubmed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
     to ribosomes. Seems to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation factor P 1 (EF-P 1).
EFP1 OR TC0398.
Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales, Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        f watch 25.5%; Score 53; DB 1; Length 597; Local Similarity 31.0%; Pred. No. 7.7; nes 13; Conservative 17. wi. no. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
PATHWAX: Protein biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the elongation factor P family.
                                                                                                                                                                                                     DR INTERPRO IPRO00095; EF GTPbind.

DR INTERPRO; IPR000161; EFTU_D2.

DR INTERPRO; IPR000161; EFTU_D2.

DR INTERPRO; IPR000178; IF2.

R INTERPRO; IPR004544; TIF_AIF-2.

R Pfam; PP00009; GTP_EFTU_D1.

R Pfam; PP001049; GTP_EFTU_D2; 1.

R TIGREAMS; TIGR00491; aIF-2; 1.

R TIGREAMS; TIGR00431; small_GTP.

R TIGREAMS; TIGR00431; small_GTP.

R ROSSITS; PS01176; IF2; FALSE_NEG.

Initiation factor; Protein blosynthesis; GTP-binding; NP RNSHIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 29 GTP (BY SIMILARITY).
84 88 GTP (BY SIMILARITY).
138 141 GTP (BY SIMILARITY).
597 AA; 65438 MW; 67CAF4D902CIBBD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQ----LKPRDL 40
the binding of the formylmethionine-tRNA tr
function along with eIF-2 (By similarity).
-!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFP1_CHLMU
09PKR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
EFP1_CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL CURSTAIN. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license largement (See http://www.isb-sib.ch/announce/or send an email to license@libs.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLI_ONCKE STANDARD; PRT; 226 AA.

C P10000; P01199; P01204; P87470; P87471; P87472; P87473; P87474;

C P10000; P01199; P01204; P87470; P87471; P87472; P87473; P87474;

C P10000; P87475; P87477; P87476; Q9521; Q92024;

T 01-TEN-1966 (Rel. 01. Created)

T 01-TEN-1991 (Rel. 01. Last sequence update)

C 01-TEN-1991 (Rel. 01. Last sequence update)

E Corticotropin-lipotropin precursor (Pro-Opiomelanocortin) (POMC)

E Contains: Corticotropin (Adrenocorticotropic hormone) (ACTH);

E Melanotropin alpha (Alpha-MSH); Corticotropin pamma (Gamma-BP); Labranochus keta (Beta-WSH); Beta-endorphin; Met-enkephalin].

C Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

C Protaccanthopteryqii; Salmoniformes; Salmonidae; Oncorhynchus.

NCSI_TAXID=8018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 92-226 FROM N.A.
MEDILINE-84280046; PubMed=6087806;
Nishizawa T., Kitahara N., Nanami H., Hara N., Kotake C., Okazaki H.,
Andoh T., Soma G.-I.;
"Heterogeneity of 3' nontranslated regions in proopiomelanocortin
(POMC) precursor mRNA of chum salmon Onchorynchus keta: polymorphism
of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
MEDLINE-89064064; PubMed=3197404;
Kitahara N., Nishizawa T., Iida K., Okazaki H., Andoh T., Soma Kitahara N., Nishizawa T., Iida K., Okazaki H., Andoh T., Soma Tabbsence of a gamma melancoyte-stimulating hormone sequence in prooptomelanocortin mRNA of chum salmon Oncorhynchus keta.";
Comp. Biochem. Physiol. 91B:365-370(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 92-226 FROM N.A.
MEDILINE-88062796; PLOMED-6095185;
Soma G.-I., Kitahara N., Nishizawa T., Nanami H., Kotake C.,
Okazaki H., Andoh T.;
"Nucleotide sequence of a cloned cDNA for proopiomelanocortin
Precursor of chum salmon, Onchorynchus keta.";
Nucleic Acids Res. 12:8029-8041(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 185;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lochem. Blophys. Res. Commun. 122:556-562(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
25.2%; Score 52.5; DB 1;
Best Local Similarity 42.4%; Pred. No. 2.4;
Matches 14; Conservative 9; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 KAALRKAHTSMV -- RNFRYGKPV - QSQLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE OF 98-112.
MEDLINE-81086168; PubMed=7447938;
                                                                                                                                                                                  EMBL; AE002306; AAF39255.1; -. PIR; B81708; B81708.
```

```
á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                  CORTICOTROPIN.
MELANOTROPIN ALPHA.
ORITCOTROPIN-LIKE INTERMEDIARY PEPTIDE.
LIPOTROPIN BETA.
LIPOTROPIN GAMMA.
                                                                                                               Blochem. Biophys. Res. Commun. 88:1249-1254(1979).
-1- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
THE DIFFERENT ACTIVE PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                Endorphin; Hormone; Cleavage on pair of basic residues; Acetylation;
                                                      SEQUENCE OF 198-226.
MEDLINE-79255548; PubMed-475783;
Kawauchi H., Tsubokawa M., Muramoto K.;
"Isolation and primary structure of endorphin from salmon pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLJ_ONCMY STANDARD; PRT; 240 AA.

G04618;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Corticotropin-lipotropin B precursor (Pro-opiomelanocortin) (POMC).
             Occurrence of a new melanocyte stimulating hormone in the salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.5%; Score 51; DB 1; Length 226; larity 36.4%; Pred. No. 5; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327CA785F69B1B24 CRC64;
                      pituitary gland.";
Biochem. Biophys. Res. Commun. 96:1508-1517(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MELANOTROPIN BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BETA - ENDORPHIN.
MET - ENKEPHALIN.
                                                                                                                                                     !- SIMILARITY: BELONGS TO THE POMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION
Kawauchi H., Adachi Y., Tsubokawa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | |: ::||:||:|
KRHSYSMEHFRWGKPIGHKRRP 116
                                                                                                                                                                                                                                                                        EMBL; M27692; AAA49426.1; ALT_INIT.
EMBL; K02613; AAA49424.1; -.
                                                                                                                                                                                                                                                                                                                    PIR; IS1080; CTONPR.
InterPro, IPR01941; Mcortin_ACTH.
Pfam, PF00976; ACTH_domain; 1.
PRINTS: PR00383; MELANOCORIN.
ProDom; PD003250; Mcortin_ACTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAHISMVRNFRYGKPVQSQLKP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Pituitary;
MEDLINE-93078794; PubMed-1448114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24982 MW;
                                                                                                                                                                                                                                                                                  EMBL; KO2613; AAA49424.1; -...
EMBL; KO2614; AAA49425.1; -...
EMBL; X01122; CAA25591.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                  98
116
1141
1141
1198
1198
226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-8022;
                                                                                                     glands.":
                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ģ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMEL cutstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ~
                                                                                                                                                                                                    MANNEAR.
-1- SIMILARITY: BELONGS TO THE POMC FAMILY.
-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-15 IS THE INITIATOR.
                                                                                            Salbert G., Chauveau I., Bonnec G., Valotaire Y., Jego P.; "One of the two trout proopiomelanocortin messenger RNAs potentially encodes new peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).

CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                      MOI. Endocrinoi. 6:1605-1613(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plk; B45359; B49559.
InterPro: IPR001941; Mcortin_ACTH.
Pfam; PF00976; ACTH_domain; 1.
ProDom; PD003250; Mcortin_ACTH; 1.
ProDom; PD003250; Mcortin_ACTH; 1.
Brdorphin; Hormone; Cleavage on pair of basic residues; Amidation; Signal; Acetylation; Pyrrollidone carboxylic acid.
SIGNAL
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

NPP 2 (BY SIMILARITY).

CORTICOTROFIN (ACTH) (BY SIMILARITY).

MELANOTROPIN ALPHA 2 (ALPHA-MSH 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
ACETYLATION (BY SIMILARITY).
AMIDATION (G-125 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPOTROPIN GAMMA (LPH-GAMMA)
(BY SIMILARITY)
MELANOTROPIN BETA 2 (BETA-MSH 2)
(BY SIMILARITY)
BETA ENDORPHIN 1 (BY SIMILARITY).
MET-ENKEPHALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 1; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLIP 2) (BY SIMILARITY).
LIPOTROPIN BETA (LPH-BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTE_SCHPO STANDARD; PRT; 506 AA.
009855; 0997V1;
01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pote Poter Protein pofil.
Pote 10 Repact protein pofil.
POTE 10 Repact protein pofil.
POTE 10 Repact protein Pofil.
POTE 11 Ascomyces pombe (Fission yeast).
ENKATYOCTA; Fungli, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetacee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4F715CE8E6424F6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 5.4;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 KRHSYSMEHFRWGKPIGHKRRP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 KAHTSMVRNFRYGKPVQSQLKP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM.;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X69809; CAA49467.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 3b.*.
Fig. 2 Conservative
Fig. 2 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
152
124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B45359; B45359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \frac{112}{124}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193
                                                                                                                                                                                              MANNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
POFB_SCHPO
```

```
SEE
                                                                                                                                                                                                                                                                                                                                                                                                             RA WEDLINE-LIABAGULI, PURBED-LIABAGUN M.A. Lyne M., Lyne R., Stewart A., RA MEDLINE-LIABAGULI, PURBED-LIABAGU, Baker S., Basham D., Bowman S., Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gentles S., Goble A., Hamlin N., Harris D., Hiddlyo J., Hodgson G., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., RA Hones L., Jones M., Harther S., McDonald S., McLean J., Annes K., Jones M., Stather S., McDonald S., McLean J., Coliver K., O'Neil S., Pearson D., Quall M.A., Rabbinovitsch E., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Ra Ra McInferford K., Rutter S., Saunders D., Quall M.A., Rabbinovitsch E., Ra Metlens I., Volckaert G., Aert R., Roben J., Grymonprez B., Weltjens I., Volckaert G., Aert R., Roben J., Grymonprez B., Weltjens I., Volckaert G., Aert R., Roben J., Grymonprez B., RA Gabel C., Fuchs M., Fitzec C., Holzer E., Moostl D., Hibbert H., Rager P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreann S., Gloux S., Lelaure V., Mctier S., Ka Daga R.R., Cruzado L., Jimnez J., Hunt C., Moore K., Hurst S.M., Adalabert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Abaga R.R., Cruzado L., Jimnez J., Rankeron S., Gloux S., Gloux S., Cadieu C., Dearen S., Gloux S., Gloux S., Hunt C., Moore K., Hurst S.M., Ra Daga R.R., Cruzado L., Jimnez J., Sanchez M., del Rey F., Benito J., Shakovski G.V., Ussery D., Barrell B.G., Nurse P., Rater 415:871-880(2002).

R. Rater 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilenticle.
                                                                                                                        Katayama S., Kitamura K., Lehmann A., Nikaido O., Toda T.; Fission yeast F-box protein Pof3 is required for genome integrity and telomere function."

Mol. Biol. Cell 13:211-224(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                         STRAIN=972;
MEDLINE=21668955; PubMed=11809834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-BOX.
WD 1.
WD 2.
WD 3.
                                                                                                                                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geneba_SPombe; SPAC29E6.01; -.
InterPro; IPR001810; F-box.
InterPro; IPR001860; WD40.
Fdam; PF00466; F-box; 1.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
PF050m; PF00018; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB061694; BAB55543.1; -. EMBL; AL136538; CAB66464.1; -. EMBL; Z66525; CAA91423.1; -. PIR; T50211; T50211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
RANGE STANDERS OF STANDERS OF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deppenmeter U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Bruegemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brutgedmann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brutzdcharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
Thiz H.-J., Gottschalk G.,
The genome of Methanosarcina mazel: evidence for lateral gene
transfer between Bacteria and Archaea.",
J. Wol. Microbiol. Biotechnol. 4:453-461(2002).
I-FUNCTION: Function in general translation initiation by promoting
the binding of the formylmethionine-tRNA to ribosomes. Seems to
function along with eIF-2 (By similarity).
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                      24.5%; Score 51; DB 1; Length 506; 44.4%; Pred. No. 12; ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAWAP; NF_00100; -; 1.

InterPro; IPR001095; EF_GTPbind.

InterPro; IPR00178; EFTU_D2.

InterPro; IPR00178; IF2

InterPro; IPR005225; Small_GTP.

InterPro; IPR004544; ITF_aTF-2.

R InterPro; IPR004544; ITF_aTF-2.

R Fam; PF00309; GTP_EFTU; 1.

R PRINTS; PR03114; GTP_EFTU_D2; 1.

R TIGRRAMS; TIGR00491; aTF-2; 1.

R TIGRRAMS; TIGR00491; aTF-2; 1.

R TIGRRAMS; TIGR00031; small_GTP; 1.

R TIGRRAMS; TIGR00031; small_GTP; 1.

R TIGRRAMS; TIGR00031; small_GTP; 1.

R TIGRRAMS; TIGR00031; Protein biosynthesis; GTP-binding;
                                                                                     CEF34D4EFFBC2E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
FE328265BBD887DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GOel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE-22120827; PubMed-12125824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable translation initiation factor IF-2.
                                                                                                                                                                                                                                                                            3 SNLRILLNKAALRKAHTSMVRNFRYGK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.0%; Score 50;
        426
464 WD
505 WD
58257 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE013490; AAM32159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64900 MW;
                                                                                                                                                                Best Local Similarity 44.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
82
  388
427
468
506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
78
132
591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFB OR MM2463.
                                                                                                                                                                                                                                                                                                                                                                                                                                       IF2P_METMA
REPEAT
REPEAT
REPEAT
SEQUENCE
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8PU78;
                                                                                                                                                                                                                                                                                                                                                                                                          IF2P_METMA
                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
```

```
Search completed: July 24, 2003, 22:04:31
Job time : 10.3214 secs
                                                                                  SEQUENCE
        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burdenformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   ä
                                                                                                                                                                                                                                                                                        MEDLINE-97079654; PubMed-8921365; 21egler S.F., Mortrud M.T., Swartz A.R., Baker E., Sutherland G.R., Burmelater M., Malligan J.T.; Molecular characterization of a nonneuronal human UNC18 homolog."; Genomics 37:19-23(1996).

- FUNCTION: INVOLVED IN THE PROTEIN TRAFFICKING FROM THE GOLG! APPRARYUS TO THE PLASMA MEMBRANE. BINDS SYNTAXINS 1A, 2, 3 BUT NOT 1-TISSUE SPECIFICITY: PLACENTA, LUNG, LIVER, KIDNEY AND PANCREAS, AS WELL AS IN PERIPHERAL BLOOD LYMPHOCYTES.

- SIMILARITY: BELONGS TO THE STREPFUNC.18/SEC1 FAMILY.
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-NEB-2003 (Rel. 41, Last annotation update)
Syntaxin binding protein 2 (Unc-18 homolog 2) (Unc-18B) (Unc18-2).
                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0%; Score 50; DB 1; Length 593; 31.1%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 NLRILLNKAALRKAHTSMYRNFRY-----GKPVQSQLKPRD 39
                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                        249 ATLDIILYDGTLKKGDTVVIGSL--GEPIRTKVRALLKPREL 288
                                     3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQ----LKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_014934.
5BE27B47B2017A2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> I (IN dbSNP:710952).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTPK_POESY STANDARD, PRT; 641 AA. P41501.
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Pathogenicity locus protein hrpk.
                                                                                                                              593 AA
31.0%; Pred. No. 21; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transport; Polymorphism.
526 526 v -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 AA; 66438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U63533; AAC50762.1; -. Genew; HGNC:11445; STXBP2.
Best Local Similarity 31.09
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.1
Matches 14; Conservative
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                      Q15833;
01-NOV-1997
                                                                                                                           STB2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRPK_PSESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                            g
                                                                                                                           q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRIN-PSS61;
MEDLINE-94100578; PubMed-8274770;
Heu S., Hutcheson S.W.;
Hutcheson S.W.;
"Nucleotide sequence and properties of the hrmh locus associated with the Pseudomonas syringae pv. syringae 61 hrp gene cluster.";
Mol. Plant Microbe Interact. 6:553-564(1993).

Tr is produced through a collabor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                              MEDLINE-94148760; PubMed-8106313; Xiao Y., Heu S., Xi J., Lu Y., Hutcheson S.W.; Alea S., Xi J., Lu Y., Hutcheson S.W.; Identification of a putative alternate sigma factor and characterization of a multicomponent regulatory cascade controlling the expression of Pseudomonas syringae pv. syringae Pss61 hrp and hrmA genes.";
Pseudomonas syringae (pv. syringae).
Bacteria; proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.0%; Score 50; DB 1; Length 641; Best Local Similarity 33.3%; Pred. No. 23; Matches 11; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U03855; AAA17653.1; -. SEQUENCE 641 AA; 67678 MW; EC098941E5B46C8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ILLNKAALRKAHTSMVRNFRYGKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 176:1025-1036(1994).
                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                  STRAIN-PSS61
```

Q8dg64 synechococo

Ognabs drosophila Og5va3 drosophila Og5va3 drosophila Og9va5 drosophila Og9va5 drosophila Og9va7 deinococcus Og9vaj3 burkholderi Og9va5 drosophila Og9va5 drosophila Og9va7 drosophila Og9ya7 drosophila Og9ya7 drosophila

095VA4 095VA3 095VA5 09S728 09S728

Q93UJ3 Q9AI37 O18150

encephalito
homo sapien
homo sapien
homo sapien

09r6/6 09hbm4 h 096b22 h 08sue7 e 09hbm3 h 000184 h 09bu65 h

agrobacteri homo sapien homo sapien

Q9VXZ7 Q9V4J5 Q8IGP7 Q8IGP7 Q8JEM4 Q9FBM4 Q9FBZ2 Q9BBZ2 Q9BBZ2 Q9BBZ3

Q8iz21 homo sapien Q83944 olive laten Q8nem5 homo sapien

Q83944 Q8NEM5

12

drosophila drosophila

099pg3 d 09w0e4 d 09hbm5 h

homo sapien

```
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85051832; PubMed-6548714;
MEDLINE-85051832; PubMed-6548714;
MEDLINE-85051832; PubMed-6548714;
MEDLINE-85051832; PubMed-6548714;
MEDLING-86.

The Meogen and N.;
The Anighly basic N-terminal extension of the mitochondrial matrix enzyme conithine transcarbamylase from rat liver.";
The Meogen and N.;
The Meogen 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
11932 MW; B739D41F19BF720D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ornithine carbamoyltransferase precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.1%; Score 179; DB 11; 92.9%; Pred. No. 5.3e-19;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
>102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 1
102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 39; Conserv
  P70518;
P70518;
01-FEB-1997 (
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
P70518
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q0117 Dos taurus
C63786 rattus norv
Q1au8 trachemys s
Q97w55 sulfolobus
C91av0 sceloporus
C91av0 sceloporus
C91av9 neisseria m
Q8av59 xenopus lae
C96570 drosophila
C52393 pseudomonas
C9746 borrelia bu
Q9xev8 bacillus ha
Q8xn77 clostridium
C99al4 bovine vira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P70518 rattus norv
Q8r1a8 mus musculu
                                                                                                                                                     July 24, 2003, 22:01:38; Search time 29.2857 Seconds (Without alignments) 361.274 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                           208
1 MLSNLRILLNKAALRKAHTS.....VRNFRYGKPVQSQLKPRDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830525
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70518
QBR1A8
QBR1U7
QG3786
Q91AW5
Q97W5
Q97W5
Q97W5
Q97W6
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         050746
09KAV8
08KNN7
099A14
                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_nvertebrate:*
sp_anmal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _rvirus:*_
_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
111
113
113
110
110
110
110
110
                                                                                                                                                                                                                                                                 US-08-765-244-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL_23:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
260
260
383
140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ummu40000000ccnu
                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.5
53.5
53.5
52.5
                                                                                                             OM protein
                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
```

102 AA

PRT;

1;

Gaps

7

0; Mismatches

MESNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKGRDL 42

a

Length 102; 1; Indels

ORNITHINE CARBAMOYLTRANSFERASE,

1;

```
61.9%;
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9IAU8
Q9IAU8;
                                                                                                                                                                                                                                                                                                               063786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9IAUB
                                                                                                ò
                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SORRARY DESTRICTION OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ή;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
"Ornithine transcarbamylase is expressed in uricotelic animals.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134841; AAF61405.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.2%; Score 144; DB 11; Length 378.6%; Pred. No. 3.9e-13; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
Strausherg R.;
Strausherg R.;
Strausherg R.;
Strausherg R.;
Strausherg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0248931; AAH24893.1; -.
HSSP; P00479; 3CSU;
InterPro; IPR0026130; Asp/Orn_Cortanf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006131; OTCace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfan: PF00155; OTCace; 1.
Pfan: PF02729; OTCace, N; 1.
TIGRFAMS; TIGR00659; OIN: Carb_tr; 1.
PROSITE; PS00097; CARBAMOXLITRNSFERASE; 1.
SEQUENCE 351 AA; 39365 MW; E6B38BB2FC779F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLSNLRILLINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30EAC2EF4AC1D71B CRC64;
                                                                                                                 QBRIAB

QBRIAB;

QBLIAB

QBLIAB;

QBLIAB;

QD.-JUN-2002 (TrEMBLrel. 21, Created)

O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Similar to ornithine transcarbamylase.

Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO0658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006131; Asp/orn_Cotranf. InterPro; IPR002592; Orn_carbtransf. InterPro; IPR006131; OTCace_O. InterPro; IPR006132; OTCace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39842 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23, Ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 78.6
nes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00100; AOTCASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBNIU7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09N1U7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                        RESULT 2
QBR1A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                           SO DE REPORTED DE LA PROPERTICIO DELLA PROPERTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
```

Length 354;

Score 114; DB 6;

Query Match

```
SEQUENCE FROM N.A.
MEDLINE-86106223; PubMed=3943133;
HOTWICH A.L., Kalousek F., Fenton W.A., Pollock R.A., Rosenberg L.E.;
Horwich A.L., Kalousek F., Fenton W.A., Pollock R.A., Rosenberg L.E.;
Targeting of pre-ornithine transcarbamylase to mitochondria:
definition of critical regions and residues in the leader peptide.";
Cell 44:451-459(1986).
EMBL, M12583; AAA41770.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Testudines, Cryptodira, Testudinoidea, Emydidae, Trachemys.
NCBI_TaxID=31138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimogirl T., Koyanagi K., Mannen H., Tsuji S.; Minogirl T., Koyanagi K., Mannen H., Tsuji S.; "Ornithine transcarbamylase is expressed in uricotelic animals."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134846; AAF61410.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.8%; Score 112; DB 11; Length 41; 61.1%; Pred. No. 2.3e-09; tive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 354;
                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLUNTS; PROGIOO; AOTCASE.
IGREAMS; TIGRO0658; orni_carb_tr; 1.
ROSITE: PSO0097; CARRAMOYITRANSFERASE; 1.
RFOUENCE 354 AA; 39958 MW; BD6A2C3AEC0F99BE CRC64;
                                                                                     1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                                    1 HELLINNAALRNGHNFVVRNFRCGQPLQDKVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AA; 4934 MW; 802465955B32374B CRC64;
                                                                                                                                                                                                                                                                                                                                           (TremBlrel. 01, Created)
(TremBlrel. 01, Last sequence update)
(TremBlrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 92; DB 13;
Pred. No. 2.6e-05;
Pred. No. 1.3e-08;
1; Mismatches 10
                                                                                                                                                                                                                                                                                       41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ornithine transcarbamylase (Fragment) Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00480; lOTH.
InterPro; IPR006130; ASP/Orn_Cotranf.
InterPro; IPR00132; Orn_carbtransf.
InterPro; IPR006131; OrCace_O.
InterPro; IPR006131; OrCace_D.
InterPro; IPR006132; OrCace_P.
Pfam; PF00185; OrCace; 1.
Pfam; PF02729; OrCace_N; 1.
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trachemys scripta elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Conservative
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel
01-NOV-1996 (TrEMBLrel
01-MAY-2000 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
```

ó

 $\sim$ 

..

Gaps

4

17; Indels

Length 356;

DB 13;

```
REDINE=98121113; PubMed=9461215;

MEDLINE=98121113; PubMed=9461215;

REDINE=98121113; PubMed=9461215;

REDINE=98121113; PubMed=9461215;

REDINE=98121113; PubMed=9461215;

REDINES W., van Staveren W., Stiekema W., Drost L.,

Redley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Redley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Redley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Redler J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,

Red Gielen J., Villarroel R., Lao N., Kavanagh T., Hempel S., Kotter P.,

Red Gielen J., Villarroel R., Deorfer R., Punk B., Meneller-Aner S.,

Red Silvey M., James R., Montfort A., Pons A., Piravandi E., Obermaier B.,

Red Silvey M., James R., Moorfes T., Jones J.D.G., Eneva T.,

Red Pelme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,

Red Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,

Redingopsis thallana.",

"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of

Red Mature 391:485-488(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRY --GKPVQS--QLKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 1286 AA: 143860 MW; F953B283C53D0DEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; 297337; CAB10276.1; -.
EMBL; Al161540; CAB78539.1; -.
                                                                                                                                                   40399 MW; 01D49CCB93E4DBD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) Hypothetical 143.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 10; L
Pred. No. 28;
8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 SNLRRMLSSSSTTKRDESLVRNLLLVSPIQLDIQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                                                                                                                           Ouery Match 26.9%; Score 56; DB 1
Best Local Similarity 38.6%; Pred. No. 6.7;
Matches 17; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1286 AA
                                                                 PRINTS, PR00100, AOTCASE.
TIGRPAMS, TIGR00658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLIRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.9%;
35.3%;
   Pfam; PF00185; OTCace; 1. Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.3.
The 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                    356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      023351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JUG9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
023351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               092069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     955E
      SO DE DE DE SO DE DE SO 
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINMATCC 35092 / DSM 1617 / P2;

MEDLINE=2133296; PubMed=11427726;

She Q. Singh R.K., Confallonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Modin N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Heikamp-de Jong I., Jeffries A.C., Wan der Cost J.,

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

The Complete Genome of S.J. S.A. 98:7835-7840(2001).

REMBL, AEO06839; AAR42533.1;

REMBL, AEO06834; TGS_dom.

PRAMI, PROSAS4; TGS_S.1.

RHYPORTHELICAL COMPLETE PROCEOME.

WHYPORTHELICAL COMPLETE PROCEOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
Subincoiri T., Koyanagi K., Mannen H., Tsuji S.;
Subincoiri T., Koyanagi K., Mannen H., Tsuji S.;
Subinci (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134844; AAF61408.1; -.
EMBL; AF134844; AAF61408.1; -.
InterPro; IPR006130; Asp/Orn_COtranf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sceloporus undulatus (Eastern fence lizard) (Skink).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguanidae; Phrynosomatinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ILLNKAA-----LRKAHISMVRNFRY----GKPVQSQ------LKPRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 17; Length 351; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
      Indels
                                                                    1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDL 40
                                                                                                          1 MLFNLRNLLNAATLRNSSKQLVQHFRSGQPTQTNINLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical GTP binding protein SS02385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.4%; Scur.
32.7%; Pred. No. 4...
... 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 AA
                                                                                                                                                                                                                                                                                                351 AA
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 32.7 tes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sceloporus.
NCBI_TaxID=8520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2287;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9IAVO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9IAV0
                                                                                                                                                                                                                                                                                                                               Q97W55
                                                                                                                                                                                                                                                                                             Q97W55
   Matches
                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9IAV0
                                                                                                                                                                                                                                                                 Q97W55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATT TO COCCOON TO THE RAP RAY OF THE PARTY AND THE RAY OF THE PARTY AND THE PARTY
                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                        ð
                                                                                                                               qq
```

; 0

Gaps

; 0

Indels

Ź

Length 1286;

```
Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
ses 12; Conserv
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HrpY protein,
HRPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              052393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
050746
ID 05074
AC 05074
DT 01-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   052393
               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCOCCOS OCT TO THE TRAIN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                   PERAIN=22131 / Serogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Whitehead M.A., Rutherford K.M., Simmonds M., Skelton J.,
"Complete DNA Sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein MGC11993.
Xenopus laevis (African clawef frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
NGBT mayth.o.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 138;
                                                                                      Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 13; Length 457; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC041284; AAH41284.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis 22491";
Nature 404:502-506(2000).
BEBL: ALGOSTSSS TABLESSS TABLESSS THE PROOFSS TABLESSS THE PROOFSS THE PROPERTY THE PROPESS THE PROOFSS THE PROPESS THE PROPESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 457 AA; 51021 MW; EE44FE225DD0039B CRC64;
01-MAR-2003 (IrEMBLrel. 23, Last annotation update)
Hypothetical protein NMA1316.
NMA1316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 RILLNKAALRKAHTSMVRNFRY-GKPVQSQLKPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54.5; D:
Pred. No. 3.9;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 LWDLRKINSKACTLHGHTSWVKNIEYDK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LSNLRILLNKAALRKAHTSMVRNFRYGK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 26.2%;
Local Similarity 42.9%;
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                         NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      096570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBAVS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8AVS9
   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mansfield J., Jenner C., Hockenhull R., Bennett M.A., Stewart R., Mansfield J., Jenner C., Hockenhull R., Bennett M.A., Stewart R., "Characterization of avrPphB, a gene for cultivar-specific avirulence from Pseudomonas syringae pv. phaseolicola which is physically linked to hrpY, a new hrp gene identified in the halo-blight bacterium."; Mol. Plant Microbe Interact. 7:726-739(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
37CS protein (Protein CS).
CG10561 OR ANON-37CS OR CS.
Drosophila lebanonensis (Fruit fly) (Scaptodrosophila lebanonensis).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Phydroidea; Drosophilidae; Scaptodrosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                         Pseudomonas syringae (pv. phaseolicola).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 54; DB 5; Length 544; 37.1%; Pred. No. 21; ive 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.0%; Score 54; DB 2; Length 769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U16817; AAA67932.1; -.
SEQUENCE 769 AA; 80021 MW; 3BDEE3F41942FBB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF003E2CBB7D6DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 VLKNFSAILFKPALPLEKLQAIRNLGYGNPVKIYL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 LVSSDSALQKAVTEQVQNVNSGKALQTDLATAD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ILLNKAALRKAHTSMVRNFRYGKPVQSQLKPRD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.4%; Pred. No. 32; ive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    050746 PRELIMINARY; PRT; 050746; 01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002937; Amino_oxidase.
InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
SEQUENCE 544 AA; 61026 MW; CF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0025668; Dleb\CG10561
                                                                                                                                                                                                                                                MEDLINE=99250256; PubMed=10231575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Race4;
MEDLINE=95178735; PubMed=7873779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
```

ö

Last sequence update)
Last annotaation update)

Created) PRT;

```
Cerrato R.R., Valle J.J., Gonzalez-Zorn B.B.; Vazquez-Boland J.J.A.;
"Clostridium novyi, nvl gene for novyilisin.";
"Clostridium novyi, nvl gene for novyilisin.";
submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ404676; CACB1998.1;
Interpro; IPR01089; Thiol_cytolysin.
Pfam; PF01289; Thiol_cytolysin.
Promp: PR01400; TACYIOLYSIN.
PROMP: PR01400; TACYIOLYSIN.
PROMP: PR007062; TAIOL_CYTOLYSIN.
SPROJERS: PS00481; THIOL_CYTOLYSINS; 1.
SEQUENCE 499 AA, 55628 MW; 6868917EBC6615F8 CRC64;
                                                                                                                                                                                                                                                                                                                            Clostridium novyi.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
             114 IQNKQILLNSAATEKATGSPARG---GKPTTTATK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 LNKGVSNEAPPLMVSNVAYGRPIYVKLE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LNKAALRKAHTSMVRNFRYGKPVQSQLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     completed: July 24, 2003, 22:07:34 ne : 34.2857 secs
                                                                                                                                                                                           (TrEMBLrel. 22, C
(TrEMBLrel. 22, I
(TrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.3;
Matches 11; Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1542;
                                                                                                                                                                                              01-0CT-2002 (
01-0CT-2002 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                  Novyilisin.
                                                                                                                                                                     Q8KNN7;
                                                                                                                                              Q8KNN7
                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search con
Job time
                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETALIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathygra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fulii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, APO01514; BAB06897.1; -.

InterPro; IPR006090; Acyl-CoA_dh_C.

InterPro; IPR006091; Acyl-CoA_dh_M.

Pfam; PF00441; Acyl-CoA_dh_M.

Pfam; PF02770; Acyl-CoA_dh_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 RILLNKAALRK-----AHTSMVRNFRYGKPVQS-------QLKPRDLC 41
                                                                                                                                   Plasmid 1p28-2.
Bacteria: Spirochaetes: Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.7%; Score 53.2; DB DC, 11, 21.8%; Pred. No. 11; tive 14; Mismatches 10; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.7%; Score 53.5; DB 16; Length 383; Best Local Similarity 42.9%; Pred. No. 17; Matches 15; Conservative 3; Mismatches 14; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic____;
burgdortgil,";
Nature 390.580-586(1997).
Nature 300.580-586(5071.1; -
EMBL; AE000786; AAC66071.1; -
TIGK; BBG23; -
TIGK; BBG23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA; 42742 MW; E20129A4F567A8C2 CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein BBG23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2002 (TrEMBLrel. 22, Last annotation update)
Short-chain-specific acyl-CoA dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches 14;
                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 21.89
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KAV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KAV8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
Q9KAV8
     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Gaps

2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQLK 36

à

ô

Gaps

ö

25.5%; Score 53; DB 2; Length 499; 39.3%; Pred. No. 27; ive 5; Mismatches 12; Indels

us-08-765-244-22.rai

```
Sequence 68, Appl
Sequence 27, Appl
Sequence 28911, Appl
Sequence 11, Appl
Sequence 5110, Appl
Sequence 50, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 6926, Appl
Sequence 6926, Appl
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
APPLICANT: HARASCO, WAYNE
APPLICANT: HARASCO, WILLIAM
TITLE OF INVENTION: WILLIAM
TITLE OF INVENTION: 79
CORRESPONDENCE ADDRESS:
ADDRESSE: MATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
COUNTRY: US
                 Sequence
Sequence
Sequence
     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 32;
                          US-08 313-553-15
US-08 -77-933-15
US-09 -25-991A-32535
US-09 914-25-68
US-09-958-858-27
US-09-958-858-27
US-09-312-758-17
US-09-312-758-14
US-09-112-758-14
US-09-112-758-14
US-09-219-933A-20
US-09-219-933A-20
US-07-846-181-5
                                                                                                                                                                                                                                    US-09-252-991A-26810
                                                                                                                                                                                                      US-09-252-991A-19085
                                                                                                                                                                                                                       US-09-328-352-6926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: BAS GEOU Version 1.5
SOFTWARE: FasteSO Version 1.5
SOFTWARE: FasteSO Version 1.5
CURRENT APPLICATION NUMBER: US/08/373,190
FILING DATE: 17-7AN 1995
CLASSIFICATION NUMBER: PCT/US93/06/35
FILING DATE: 16-JUL-1993
APPLICATION NUMBER: PCT/US93/06/35
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: REGISTATION NUMBER: 34,235
REGISTRATION NUMBER: 41956-PCT-US
REGISTRATION NUMBER: 41956-PCT-US
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                           US-07-845-989-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92;
                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08373190 Patent No. 5851829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 32 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                 US-08-373-190-29
Query Match
 Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 42, Appl
Sequence 18053, A
Sequence 2, Appl 1
Sequence 5, Appl 1
Sequence 5, Appl 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl
                                                                                     July 24, 2003, 22:02:54; Search time 20.9881 Seconds (without alignments) 86.686 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1
Sequence 3
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3
Sequence 2
Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1
Sequence 1
Sequence 1
                                                                                                                                          US-08-765-244-22
217
1 MLSNIRILILNKAALRKAHTS.....NFRYGKPVQSQVQLKPRDLC
                                                                                                                                                                                                                                                                         328717
                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-438-190A-29
US-08-438-190A-29
US-09-287-111-29
US-09-556-111-29
US-09-556-111-29
US-09-252-991A-32812
US-08-252-991A-32812
US-08-252-991A-32812
US-08-252-991A-32812
US-08-68-2
US-08-68-2
US-09-107-532A-5399
US-09-107-532A-5399
US-09-107-532A-5399
US-09-107-10-98
PCT-US-05-10-98
PCT-US-07-10-98
US-09-732-210-195
US-09-732-210-195
US-09-002-567B-1
US-09-188-811-2
US-09-571-347-1
US-09-188-811-2
US-09-571-347-1
US-09-188-811-2
US-09-571-347-1
US-09-552-991A-29653
US-09-552-17-16
US-09-552-77-16
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444
0000
...44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                               OM protein
                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
```

```
Sequence 29, Application US/09287145A
| Sequence 29, Application US/09287145A
| Patent No. 6072036
| GENERAL INFORMATION:
| APPLICANT: MARASCO, WAYNE
| APPLICANT: HASEITINE, WILLIAM
| TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
| TITLE OF INVENTION: PROTEINS
| NUMBER OF SEQUENCES: 78
| CORRESPONDENCE ADDRESS: 78
| ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS G. STREET: 130 WATER STREET
| STREET: 130 WATER STREET
| CONTY: DOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
                                                                                                                                                                           OPERATION SISTEM: PC-UDS/MS-LUGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/08/350,215
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: ELSENSTEIN, RONALD I
REGISTRATION NUMBER: 30628
REFERENCE/POCKET UNMBER: 41956-CP3
TELEPHONE: (617) 523-3440
TELEPHONE: (617) 523-3440
TELERA: (617) 523-3440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,145A
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.4%; Score 92; DB 3; 161.3%; Pred. No. 9.2e-08; tive 2; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190
                                                                            ZIP: 02109
COMDUTER READABLE FORM:
COMPOUT TYPE: Floppy disk
COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/CABORT INFORMATION:
NAME: EISENGTEIN, RONALD I
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.39
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                 MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
                                                                         02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-287-145A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-350-215-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                 ö
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                 ö
                                                                                                                                                                                            US-08-438-190A-29

Sequence 29, Application US/08438190A

Patent No. 5965371

GENERAL INFORMATION:
APPLICANT: HASELINE, WILLIAM
ITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
ITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN

STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/08350215
Patent No. 6004940
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE A.
APPLICANT: RICHARDSON, JENNIFER
TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGEMOUS
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
Best Local Similarity 61.3%; Pred. No. 9.2e-08;
Matches 19; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 92; DB 2; Le
Pred. No. 9.2e-08;
2; Mismatches 10;
                                                                     1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                               1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATORNEYAGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRAATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-438-190A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-350-215-29
                                                                                                                                                                                  RESULT 2
                                                                                                                g
                                                                       á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

ó

0; Gaps

```
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILER REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32812
                                                                                                             APPLICANT: Geselschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Brocker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Condition of Petra
APPLICANT: Globerg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Reichenbach, Hans
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: heteropolyketide compounds
TITLE REPERENCE: POT/US 99/23355
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
ERRLIER FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (451); (OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.4%; Score 53; DB 4; Length 457; ilarity 34.4%; Pred. No. 4.1; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ILLNKAALRKAHTSMVRNFRYGKPVQSQVQLK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32812, Application US/09252991A Patent No. 6551795
                                                        Sequence 42, Application US/09413814
Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.5
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
                                S-09-413-814-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-413-814-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δŽ
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MARKSCO, WAYNE
HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
PROFEINS
                                                                                                                                                                                                      Length 32;
                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.4%; Score 92; DB 4; Length 32; 61.3%; Pred. No. 9.2e-08; 1ve 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 21-Apr-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                  Score 92; DB 3; 1
Pred. No. 9.2e-08;
2; Mismatches 10,
                                                                                                                                                                                                                                                                                      1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                    1 MLFNLRXXLNNAAFRHGHNFWVRNFRCGOPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: «UNALOWN»

ATTORNEY/AGENT INFORMATION:
NAME: BISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1inear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/438,190
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09556111
Patent No. 6329173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 WATER STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 523-34C
TELEFAX: (617) 533-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 32 amino acids TYPE: amino acid
                                                 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MASSACHUSETTS
                                                                                                                                                                                                  42,4%;
ilarity 61.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUSHMAN
TELERAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
                                                                                           32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                         ; TYPE: amino acid
; TOPOLOGY: linear
US-09-287-145A-29
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-556-111-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-556-111-29
                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

ó

ó

g

.; (1

```
Query Match 23.5%; Score 51; DB 1; Length 1169;
Best Local Similarity 25.5%; Pred. No. 28;
Matches 14; Conservative 12; Mismatches 15; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                       2 LSNLRILLN------KAALRKAHTSMVRNFRYG---KPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KAALRKAHTSMVRNFRYG----KPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ILZUKA, TOSHIHIKO
APPLICANT: TRGAWA, MICHITO
APPLICANT: TRGAWA, MICHITO
APPLICANT: TRGAWA, MICHITO
APPLICANT: TRGAWA, MICHITO
APPLICANT: MIXAKE, TOSHIRO
TITLE OF INVENTION: ONCEL BACILLUS STRAIN AND HARWFUL
TITLE OF INVENTION: ONCEANISM CONTROLLING AGENTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOW, SPLVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
LIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: TOSPY disk
COMPUTER: DATOR IN STATE:
COMPUTER: DATOR IN STATE:
APPLICATION NUMBER: US/O8/880,685
FILING DATE: 13-0CT-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 2220
TELEFAX: 24885 ORAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERSTICS:
LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%; Score 51; DB 25.5%; Pred. No. 28; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08880685
Patent No. 5834296
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 23.5
Best Local Similarity 25.5
Matches 14; Conservative
                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-542-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LSNLRILLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-880-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-880-685-2
                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                           Sequence 18053, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
RATC J. RUBenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
ABUDICANT:
REPRINCE:
107196.136
CURRENT FILING DATE:
1999-02-18
PRIOR PAPLICATION NUMBER:
US 60/074,788
PRIOR FILING DATE:
1998-02-18
PRIOR FILING DATE:
1998-02-18
PRIOR FILING DATE:
1998-02-18
PRIOR FILING DATE:
1998-07-27
NUMBER OF EXQ ID NOS:
33142
LENGTH:
218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08542921

Sequence 2, Application US/08542921

Sequence 2, Application US/08542921

Sequence 3, Application US/08542921

Settlicant: IIZUKA, TOSHIHIKO

APPLICANT: ARAL, SATOSHI

APPLICANT: ARAL, SATOSHI

APPLICANT: NIIZEKI, MASATSUGU

APPLICANT: NIZEKI, MASATSUGU

TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL

TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS

NUMBER OF SEQUENCES:

ADDRESSEE: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1155 S. JEFFERSON DAVIS HIGHMAY, FOURTH FLOOR

STATE: VIRGINIA

COMPTRY: USA

ZIP: Z2202

COMPTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 4; Length 218;
Pred. No. 2.4;
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLSNLRILLNKAALRK-----AHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIBM FC compatible
COMPUTER: PIBM FC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/542,921
CLIASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/294
FILING DATE: 14-0CT-1994
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F
REFERENCE/POCKET NUMBER: 24,618
REFERENCE/POCKET NUMBER: 49-209-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.0%;
Best Local Similarity 33.3%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NE: (703) 413-3000
(: (703) 413-2220
248855 OPAT UR
                                                              -09-252-991A-18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
TELEX: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

.; ;

d

```
Sequence 18693, Application US/0925291A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: 107166.136
GURRENT PELLING DATE: 1999-02-18
PRIOR PRILING DATE: 1999-02-18
PRIOR PILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1999-07-18
PRIOR FILLING DATE: 1999-07-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.5; DB 4; Length 523; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%; Score 49.5; DB 4; 40.7%; Pred. No. 5.6;
                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...208;
SEQUENCE DESCRIPTION: SEQ ID NO: 5399;
US-09-107-532A-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNET/AGENT INFORMATION:
NAME: AFINIGELO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NKAALRKAHISMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 NKAA------ONFRYGKPFTPELE 76
                                                                                               2IP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5399:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
                                  CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 40.7 Matches 11; Conservative
                                                                                                                                                                                                              SOFTWARE: ASCII
                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-18693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pseudo
US-09-252-991A-18693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5399, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FOR SEQUENCES: 7310
359 LSNLQILVNYQTNGSAWRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINVQNNDI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LSNLRILLN------KAALRKAHTSMVRNFRYG---KPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 1169;
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Indels
                                                                                                                                                                                                                                                                                                                                                                            : OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
APPLICANT: ARAI, SATOSHI
APPLICANT: MIZEKI, MASATSUGU
APPLICANT: MITZEKI, MASATSUGU
APPLICANT: MITZEKI, MASATSUGU
TILLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NAMER: US/08/880,684 FILING DATE: 23-JUN-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 28;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/542,921
FILING DATE: 13-0CT-1995
APPLICATION NUMBER: JP 276082/94
FILING DATE: 14-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24,618
ER: 49-209-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             Sequence 2, Application US/08880684 Patent No. 5837526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 24855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.5%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: protein US-08-880-684-2
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-107-532A-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22202
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOPOLOGY:
                                                                                   US-08-880-684-2
```

δ g

```
TITLE OF INVENTION: Compositions and Methods Based Upon the Tuberous Sclerosis-1 (TSC-1) Gene and Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: U.S.

ZIP: 20004-1008

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTY
COMPUTER: US/09/950,046A
FILING DATE: 12-Sep-2001
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLSNLRILLINKAALRKAHTSMV----RNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                         NAME: SANZO, MICHAEL A.
REGISTRATION NUMBER: 36,912
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
TELEPHONE: (202) 639-6585
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.5; DB 4; Dred. No. 48; 9; Mismatches 19;
                                                                              ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-950-046A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: July 24, 2003, 22:08:53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.8%;
Best Local Similarity 29.8%;
Matches 14; Conservative
                                            NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search cor
Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                      APPLICANT: Kwiatkowski, David J.
APPLICANT: Sampson, Julian R.
APPLICANT: Sampson, Julian R.
APPLICANT: Povey, Sue
APPLICANT: van Slegtenhorst, Marjon
APPLICANT: was Slegtenhorst, Marjon
APPLICANT: Walley, Dicky
TITLE OF INVENTION: Compositions and Methods Based U
TITLE OF INVENTION: Sclerosis-1 (TSC-1) Gene and Gene Product
NUMBER OF SEQUENCE: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
CIT: Washington
STATE: D.C.
COUNTRY: U.S.
      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                1 MLSNLRILLNKAALRKAHTSMV----RNFRYGKPVQSQVQLKPRDL 42
      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR1331/42002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.5;
Pred. No. 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kwiatkowski, David J.
Sampson, Julian R.
Povey, Sue
van Slegtenhorst, Marjon
Halley, Dicky
                                      6 RILLNKAALRKAHTSMVRNFRY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09950046A Patent No. 6548258 GENERAL INFORMATION:
                                                                                                                                                                  ; Sequence 2, Application US/09457708
; Patent No. 6326483
    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20004-1008
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.8
Best Local Similarity 29.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-950-046A-2
                                                                                                                            RESULT 14
US-09-457-708-2
  Matches
                                        ŏ
                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
July 24, 2003, 22:01:38; Search time 30.7143 Seconds (without alignments) 361.274 Million cell updates/sec
                                                                                                                                                                                       US-08-765-244-22
217
1 MLSNLRILLNKAALRKAHTS.....NFRYGKPVQSQVQLKPRDLC 43
                                                                                                                                                                                                                                                                                                                                                                   830525
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_tung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_23:*
                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                 Run on:
```

# sp\_organelle:\* sp\_phage:\* sp\_plant:\* sp\_vordent:\* sp\_vordent:\* sp\_vordent:\* sp\_vordent:\* sp\_vordent:\* sp\_vordent:\* sp\_vordent:\* sp\_arching:\* sp

Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	total score distribution.
Pred. No. is the number of res	score greater than or equal to	and is derived by analysis of the total score distribution,

	Description	P70518 rattus norv	Q8rla8 mus musculu	Q9nlu7 bos taurus	Q63786 rattus norv	Q9iau8 trachemys s	Q9iav0 sceloporus	023351 arabidopsis	Q97w55 sulfolobus	Q9yhy9 gallus gall	Q9z635 streptococc	Q91mn3 arabidopsis	044679 caenorhabdi	QBavs9 xenopus lae	096570 drosophila	Q9gpg3 drosophila	Q9w0e4 drosophila
SUMMARIES	DI	P70518	Q8R1A8	Q9N1U7	963786	Q91AU8						O9LMN3		QBAVS9	09.6570	Q9GPG3	Q9W0E4
	Query Match Length DB	102 11	351 11	354 6	41 11	354 13				354 13				457 13	544 5	866 5	866 5
df	Query Match 1	91.7	75.6	59.9	54.8	48.8	32,3	28.1	27.6	26.3	25.8	25.6	24.9	24.9	24.9	24.9	24.9
	Score	199	164	130	119	106	70	61	9	57	26	55.5	54	54	54	54	24
	Result No.	П	8	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16

·;

Gaps

ö

Query Match
91.7%; Score 199; DB 11; Length 102;
Best Local Similarity 97.6%; Pred. No. 9e-22;
Matches 41; Conservative 0; Mismatches 1; Indels

g S

Q81rh0 drosophila Q81rh1 drosophila Q8456 coxiella bu Q9445 drosophila Q91909 oryza sativ Q92c64 yersinia pe Q80dd rycsania pe Q91ug9 neisseria m	SIN	PRT; 102 AA.  reated) ast sequence update) ast annotation update) e precursor (Fragment).  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.  714; J., Peterson G., Hudson P.J., tension of the mitochondrial matrix lase from rat liver.";  ANSFERASE; 1. POTENTIAL. ORNITHINE CARBAMOYLTRANSFERASE. B739D41F19BF720D CRC64;
	alignment	Att; 102 A ated; t sequence t annotatio precursor ( raniata; Ve clurognathi , Peterson nsion of th se from rat tranf.  SFERASE; 1. TENTIAL. NITHINE CAR
081RH0 081RH1 020G64 020G64 091GD7 091GD7 092C64 09	ALIC	UNARY; PRT; 102  Lizel. 02, Created)  Lizel. 02, Last sequency  Lizensferase precursor  (Rat). Chordata; Craniata; Chordata; Craniata; Chordata; Craniata; Rodentia; Sciurognat  L., Mercer J., Peterso  terminal extension of  ranscarbamylase from r  46(1984). Chordata; Spyorn_Cotranf. Sourcace_P. CARBAMOVILTRANSFERASE; CA
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		02, 02, 02, fera data ntia ntia ntia ntia ntia ntia ntia n
10053 10075 74271		MINARY;  BLTEL. 02, Cre BLTEL. 23, Las BLTEL. 23, Las BLTEL. 23, Las FILLS. CAR ALTON CRATE  To Chordata; C  A; Rodentia; S  Chordata; C  A; Rodentia; S  Chordata; C  A; Rodentia; S  A; Rodentia; S  A; Chordata; C  A; Chor
44444444444444444444444444444444444444		PRELIMIN 1997 (TrEMBLE 2003 (TrEMBLE 2005 (TrEMBLE 2005 (TrEMBLE 2004 (T
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		DIT 1  518  P70518  P70518  P70518  P70518  P70518  O1-FEB-1997 (TTEMBLTE1. 02, Cre O1-FEB-1997 (TTEMBLTE1. 23, Las O1-MAR-2003 (TTEMBLTE1. 23, Las O1-MAR-2003 (TTEMBLTE1. 23, Las OTHILTHOR CATADAMONITHENSFERASE RATUS DOTORY (RAI). EUKARYOTA: METAZOA; CHORDIA; SAGOENCE FROM N.A. MEDLINE-8051832; Pubmed-654871 MCINTYRE P., Graf L., Mercer J., Rhghly basic N-terminal extensyme crnithine transcarbamyla FEBS. Left. 177.41-46(1984). FEBS. P00480; 10TH. HSSP; P00480; 10TH. HSSP; P00480; 10TH. FEBS. TRANSCACE.N: 11. PROSITE: PS00097; CARBAMONITRAN SIGNAL 33 > 102 OR CHAIN 33 > 102 OR NON. TER
11112222222222222222222222222222222222		PP PS SULT

ó

Gaps

;; 0

RESULT Q8R1A8

```
SEQUENCE FROM N.A.
MEDLINE=86106223; PubMed=3943133;
MEDLINE=86106223; PubMed=3943133;
MEDLINE=86106223; PubMed=3943133;
MIDIANE=8610624; F., Fenton W.A., Pollock R.A., Rosenberg L.E.;
Targeting of pre-cruithine transcarbamylase to mitochondria:
definition of critical regions and residues in the leader peptide.";
Cell 44:451-459(1986).
EMBL, MI2583; AAA41770.1; -.
NON_TER 41
A1
SEQUENCE 41 AA, 4934 MW; 802465955B32374B CRC64;
                                                                                                                                                                                                                                        01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
ornithine transcarbamylase (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Testudines, Cryptodira, Testudinoidea, Emydidae, Trachemys.
NCBI_TaxID=31138,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
"Ornithine transcarbamylase is expressed in uricotelic animals.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134846; AAF61410.1; -.
  Pred. No. 7.1e-11;
; Mismatches 10; Indels
                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.8%; Score 119; DB 11;
66.7%; Pred. No. 2.8e-10;
tive 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 AA
                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P00480; 10TH.
InterPro; IPR005130; Asp/Orn_COtranf.
InterPro; IPR002529; Orn_carbtransf.
InterPro; IPR005131; Orcace_O.
InterPro; IPR006132; OrCace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23, ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trachemys scripta elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 66.7
Matches 24; Conservative
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00100; ACTCASE
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
  Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                     063786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9IAU8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9IAU8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                              ò
                                                                                                 q
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                           08R1A8;

01-JUN-2002 (TERMELrel. 21, Last sequence update)

01-JUN-2002 (TERMELrel. 21, Last sequence update)

01-MAR-2003 (TERMELrel. 23, Last annotation update)

01-MAR-2003 (TERMELrel. 23, Last annotation update)

01-MAR-2003 (Mouse).

Mus musculus (Mouse).

Eukaryota, Netazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimogiri T., Koyanagi K., Mannen H., Tsuji S.; "Ornithine transcarbamylase is expressed in uricotelic animals."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134841; AAF61405.1; -. HSSP; P00480; 10TH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 164; DB 11; Length 3
Pred. No. 5.9e-16;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; P004793; AAH24893.1; -.
HSSP; P00479, 3CSU.
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006130; Dap/Orn_COtranf.
InterPro; IPR006131; Orn_carbtransf.
InterPro; IPR006131; OrCace_O.
InterPro; IPR006132; OrCace_P.
Pfam; PF00108; OrCace; I.
Pfam; PF02129; OrCace; I.
TIGRFAMS; TIGR00658; Orni_carb_tr; I.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; I.
SEQUENCE 351 AA; 39365 MW; E6B3BBB2FC779F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLSNLRILLNNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO06130; Asp/orn_cotranf.
InterPro; IPRO06130; Orn_carbtransf.
InterPro; IPRO06131; Ordcace_O.
InterPro; IPRO06131; Ordcace_O.
Pfam; PRO0185; Ordcace_N.
Pfam; PRO729; Ordcace_N.
PRINTS; PR00100; AOTCASE.
TIGREAMS; TIGRO0658; Orn_carb_tr; 1.
PROSTIE; PS000097; CARBAMOYLTRANSFERASE; 1.
SEQUENCE 354 AA; 39842 MW; 30EAC2EF4ACID71B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
                                                                                  351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 130;
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-MAR-2003 (TrEMBLrel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9N1U7
                                                                              Q8R1A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

RESULT Q9N1U7

SO DRANGE SELECTION OF STREET OF STR

δŏ g

ö

Gaps

ö

Indels

ä

Length 41;

```
Length 354;
                                          BD6A2C3AEC0F99BE CRC64;
                                                                               Score 106; DB 13;
Pred. No. 2.7e-07;
TIGREAMS; TIGRO0658; Orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
SEQUENCE 354 AA; 39958 WW; BD6A2C3AECO;
                                                                               48.8%;
52.4%;
                                                                                  Query Match
Best Local Similarity
```

œ œ

E., Obermaler

δ g 

```
Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermale Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T., Balme K., Bense V., Rechman S., Ansorge W., Cooke R., Berger C., Schueller C., Chalwatzis N., Analysis of 1.9 Mo of contiguous sequence from chromosome 4 of Arabidopsis thaliana."; Nature 391:485-488(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                             107 SNLRRMLSSSTTKRDESLVRNLLLVSPIQLDIO 140
                                                                                                                                                                                                                                                                                                                           3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z
                                                                                                                                                                                                                                                                                                                                                                                                                                    351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 10, (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.6
Best Local Similarity 34.6
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulfolobus solfataricus
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
----- 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9YHY9;
01-MAY-1999 (
01-MAY-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9YHY9
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
097W55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q9YHY9
        õ
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 K L L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=98121113; PubMed=9461215;

MEDLINE=98121113; PubMed=9461215;

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,

Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Wedler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,

Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,

Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,

Silvey M., James R., Montfort A., Pons A., Pulgdomenech P., Douka A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Af4G14970.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                   OTC.
Sceloporus undulatus (Eastern fence lizard) (Skink).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 13; Length 356;
Pred. No. 0.063;
6; Mismatches 18; Indels
      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRY--GKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02/29; OLCASE.
PRINTS; PR0100; AOTCASE.
TIGRFAMS; TIGR00658; Orn1_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                     42
                                 1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 143.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1286 AA
                                                                                                                                           356 AA
      Mismatches
                                                                                                                                                                        Created)
                                                                                                                                           PRT;
      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%;
Similarity 40.9%;
18; Conservative
                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                   Ornithine transcarbamylase.
    22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Sceloporus.
NCBI_TaxID-8520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      023351
                                                                                                                                                           Q9IAVO;
                                                                                                                                         Q9IAV0
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 023351
                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                            Q9IAV0
```

d

á

```
C STRAIN—ATCC 35092 / DSM 1617 / P2;

KX MEDLINE=21332296; PubMed=11427726;

RA Mayez M.J., Chan-Weiher C.C.-T., Clausen I.G., Curtis B.A.,

RA Awayez M.J., Chan-Weiher C.C.-T., Clausen I.G., Curtis B.A.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RA Garrett R.A., Medina Solfataricus P2.";

RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RT Proc Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

RE MEL; AE006839; AAK42533.1; -..

InterPro; IPRO04095; TGS_dom.

R Pfam; PPO2844; TGS; 1.

KW Hypothetical protein; Complete proteome.

SEQUENCE 351 AA; 39916 MW, 046A96BF004865DE CRC64;
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
m
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ILLNKAA-----LRKAHTSMVRNFRY----GKPVQSQVQ------LKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                    Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.6%; Score 60; DB 17; Length 351; 34.6%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                   Hypothetical protein.
SEQUENCE. 1286 AA; 143860 MW; F953B283C53D0DEE CRC64;
                                                                                                                                                                                                                                                                                                        Indels
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 297337; CAB10276.1; -.
EMBL; AL161540; CAB78539.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical GTP binding protein SSO2385.
                                                                                                                                                                                                                                28.1%; Score 61; DB 10; L. 38.2%; Pred. No. 5.8; tive 7; Mismatches 14;
```

ij

```
Query Match
Best Local Similarity
"-+rhes 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C14C6.13
                                                                                                                                                                                                                                                                                    09LMN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      044679;
                                                                                                                                                                                                                                                                O9LMN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                044679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
044679
                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                            O9LMN3
                                                                                                                   ò
                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=BREED WHITE LEGHORN; TISSUE=Kidney;

X MEDLINE=99011321; Pubmed=9792920;

Shimogiri T., Kono M., Mannen H., Mizutani M., Tsuji S.;

Chicken ornithine transarbamylase gene, structure, regulation, and stromosomal assignment: repetitive sequence motif in intron 3

T chomosomal assignment: repetitive sequence motif in intron 3

RT regulates this enzyme activity.";

T is alochem. 124:962-971(1998).

DR EMBL; AF065639; AAD33083.1;

DR EMBL; AF065631; AAD33083.1;

DR EMBL; AF065631; AAD33083.1;

DR EMBL; AF065635; AAD33083.1;

DR EMBL; AF065631; AAD33083.1;

DR EMBL; AF065635; AAD33083.1;

DR EMBL; AF065631; AAD33083.1;

DR EMBL; AF065631;

AAD33083.1;

DR EMBL; AF065631;

AAD33083.1;

AAD3308
                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=99395043; PubMed=10464207;
Morona Jr., Morona R., Paton J.C.;
Streptococcus pneumoniae types belonging to serogroup 19.";
EMBL; AR105116; AAD19925-15;
InterPro; IPR001286; Glyco_trans_1.
Pfam, PF00534; Glyco_trans_1.
Transferase.
SEQUENCE 369 AA, 43229 WW; FOFCFD5C106AC8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.3%; Score 57; DB 13; Length 354; llarity 40.5%; Pred. No. 5.5; Conservative 4; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 AA; 40245 MW; 20447180BAD9D4ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 AA; 43229 MW; FCFCFD5C106AC8BE CRC64;
  01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Ornithine transcarbamylase precursor (EC 2.1.3.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10, Created)
10, Last sequence update)
23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO0658; Orni_carb_tr; 1.
PROSITE; PSO0097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005130; Asp/orn_Cotranf.
InterPro; IPR002292; Orn_carbtransf.
InterPro; IPR006131; Orcace_0.
InterPro; IPR006132; Orcace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Cre
01-MAY-1999 (TrEMBLrel. 10, Las
01-MAR-2003 (TrEMBLrel. 23, Las
Putative glucosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                              NCBL_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q92635
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brasslcales, Brassicaceae, Arabidopsis.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. Columbia;
Liu S.X., Sakano H., Yu G., Etgu P., Lee J.M., Lenz C., Pham P.,
Liu S.X., Sakano H., Yu G., Etgu P., Chin C., Chin E., Ching M.,
Goldsmith A., Byun E., Chao A., Liu A., Smith A., Vayaberg M., Altafi H.,
Brooks S., Buehher E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
Federspiel N.A., Theologis A.,
The sequence of BAC Fifet from Arabidopsis thaliana chromosome 1.",
Submitted (JUL-2000) to the EmbL/GenBank/DDBJ databases.
EMBL; AC036104; AAF81364.1;
SEQUENCE 454 AA; 50928 MW; 70BC2ACCC9DBEDCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 25.6%; Score 55.5; DB 10; Length 454; I Similarity 45.2%; Pred. No. 12; 14; Conservative 5; Mismatches 11; Indels 1;
   Length 369;
Score 56; DB 2; Length 369
Pred. No. 8.1;
9; Mismatches 14; Indels
                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                     01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
F16F4.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 33.8 kDa protein.
                                                                                                                  4 NIRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC
                                                                                                                                                                          NVHKVLVRLGIKKSDMSMT ----YIKYAENQVHLSPEDVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Bristol N2;
David M., Wohldmann P., Bauer C., Antoniou B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 KAALRKAHT-SMVRNFRYGKPVQSQVQLKPR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
```

ö

Gaps

0

Indels

20;

5; Mismatches

DB 5; Length 544; 25;

```
1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLK 38
                                                                                                                              Query Match 24.9%; Score 54; Best Local Similarity 34.2%; Pred. No. Matches 13; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aminopeptidase.
SEQUENCE 866
                                                                                                                                                                                                                                                           Q9GPG3
                                                                                                                                                                                                                                                                        O9GPG3
                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                Q9GPG3
      SUBBREARS
                                                                                                                                                                              δ
                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY.1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 17, Last annotation update)
01-MAY-1999 (TrEMBLrel. 17, Last annotation update)
37CS protein (Protein CS).
CG10561 OR ANON-37CS OR CS.
Drosophila lebanonensis (Fruit fly) (Scaptodrosophila lebanonensis).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7225;
                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein MGC11993.
Senopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordaus Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tatarenkov A., Saez A.G., Ayala F.J.; "A compact gene cluster in drosophila: the unrelated Cs gene is
                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 13; Length 457;
Pred. No. 20;
3; Mismatches 12; Indels
                                                                                                                                                  Score 54; DB 5; Length 300;
Pred. No. 13;
                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041284; AAH41284.1; ...
Hypothetical protein.
SEQUENCE 457 AA; 51021 MW; EE44FE225DD0039B CRC64;
"The sequence of C. elegans cosmid C14C6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL, AR039051; ARB94269.1; -, Wornepp, C14C6.13; CE08168. Hypochetical protein.
                                                                                                                al protein.
300 AA; 33753 MW; 227DF298FFD8AC83 CRC64;
                                                                                                                                                                                                              2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                457 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 AA.
                                                                                                                                                                         10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LSNLRILLNKAALRKAHTSMVRNFRYGK 29
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BEIRUT;
MEDLINE-99250256; PubMed-10231575;
                                                                                                                                                 24.9%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.9%;
Best Local Similarity 46.4%;
Matches 13; Conservative
                                                                                                                                                              Best Local Similarity 31.4 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                PRELIMINARY;
                                  SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus,
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Embryo;
                                                                                                                            SEQUENCE
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      096570;
                                                                                                                                                                                                                                                                                           Q8AVS9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           096570
                                                                                                                                                                                                                                                       RESULT 13
Q8AVS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
096570
 ò
                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           å
```

```
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Puromycin-sensitive aminopeptidase.
PSA OR CG1009.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.9%; Score 54; DB 5; Length 866; Best Local Similarity 33.3%; Pred. No. 42; Matches 15; Conservative 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LSNLRILLNKAALRKAHTSMVRNF-RYGK----PVQSQVQLKPRD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schulz C., Perezgasga L., Fuller M.T.;
Schulz C., Perezgasga L., Fuller M.T.;
"Functional analysis of a Drosophila puromycin-sensitive
aminopeptidase gene.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF327435, AAG48733.1;
EMBROPS; MI.010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 AA; 99450 MW; 907F7D14404760AB CRC64;
332 VLKNFSAILFKPALPLEKLQAIRNLGYGNPVKIYLAYK 369
                                                                                                                                                                  866 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: July 24, 2003, 22:07:37 Job time : 33.7143 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001930; Ala peptase.
InterPro; IPR002114; HPL SerP_site.
InterPro; IPR006025; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIMIS: PRO0756; ALADIPLASE.
PROSITE, PS00589; PTS_HPR_SER; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01433; Peptidase_MI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0035226; Psa.
                                                                                                                                                           PRELIMINARY;
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

July 24, 2003, 21:59:48; Search time 7.67857 Seconds (without alignments) 263.350 Million cell updates/sec Run on:

US-08-765-244-22
217
1 MLSNLRILLINKAALRKAHTS.....NFRYGKPVQSQVQLKPRDLC 43 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	rattus no	P11725 mus musculu	00480 homo sapien		Q8pu78 methanosarc	31326 rana catesb			90640 gallus gall			O9pkr6 chlamydia m		Q09855 schizosacch							Q97wh0 sulfolobus	9z136 rattus norv		_	04439 saccharomyc			P11716 oryctolagus			P59483 buchnera ap	16 anabaena	P00723 kluyveromyc
		ă	Δ,	<u>a</u>	ā	ā	ã	ď	ä	Δ.	ä	Ö	ď	ä	Δ	ŏ	ă	ŏ	ä	ă	ŏ	Ö	à	ä	ă	Ď,	ă	ρí	Д	Ď,	ሲ	Ď,	ď	'n,	ŭ
		1																																	
SUMMARIES		TD .	OTC_RAT	OTC_MOUSE	OTC_HUMAN	IF2P_METAC	IF2P_METMA	OTC_RANCA	RR2_LOTJA	HEMN_SALTY	KF4A_CHICK	OTC_PIG	CGS5_YEAST	EFP1_CHLMU	NARX_ECOLI	POFB_SCHPO	YM37_YEAST	C9DA_BACTP	TRB2_SULSO	LAFU_VIBPA	SR68_CANFA	PRCA_ANASP	RA50_SULSO	TSC1_RAT	TSC1_HUMAN	HEMN_ECOLI	MYS5_YEAST	YHOO_YEAST	RYR1_PIG	RYR1_RABIT	RYR1_HUMAN	R37A_SCHPO	SYR_BUCBP	PRCA_ANAVA	BGAL_KLULA
		BB		<b>-</b>	-	Н	Н	Н	7	1	-	•							-			•									Н		<del>(  </del>		Ä
		Length	354	354	354	597	591	350	236	457	1225	328	435	185	598	506	705	1169	429	330	622	662	864	1163	1164	457	1219	1345	5035	5037	5038	88	578	647	1025
ф	Query	Match	91.7	75.6	65.0	27.2	25.8	25.3	24.9	24.9	24.9	24.4	24.4	24.2	24.0	23.5	23.2	23.5		-	23.0	23.0	22.8	22.8	22.8	22.6	22.6	22.6		22.4	22.4	22.1	22.1	22.1	22.1
		Score	199	164	141	ത	26	22	54	54	54	က က	23	52.5	52	51	51	21	50.5	20	50	20	9	49.5	σ.	49	49	ϭ,	ω.	æ	48.5	48	48	48	<b>4</b> 4
	Result	NO.	1	(7)	m	4	ın	Q	7	φ .	σ,	10		12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q8k9g1 buchnera ap P20740 qallus qall	Q66802 ébola vírus P05733 schizosacch	Q9v122 pyrococcus O59219 pyrococcus	Q9ugi8 homo sapien P47226 mus musculu	P10581 zea mays (m P24607 pseudomonas	065952 canine aden 096685 canine aden
Y376_BUCAP OVOS_CHICK	RRPL_EBOSM R37B_SCHPO	PSMA_PYRAB PSMA_PYRHO	TES_HUMAN TES_MOUSE	RPOP_MAIZE T801_PSESH	VCOM_ADECC VCOM_ADECR
333 1473	2210 90	260 260	421	1098	421
21.9	21.9	21.7	21.7	21.7	21.4
47.5	47.5	47	7.4 7.4	46.5	46.5 46.5
34 35	36 37	8 6 6 6	4 4 1	4 4 2 8	44 45

## ALIGNMENTS

。 日:	OTC_RAT ID OTC_RAT STANDARD; PRT; 354 AA.	
S E	PU0481; Q63407;	
15	21-JUL-1986 (Rel. 01, Last sequence update)	
Ę	16-OCT-2001 (Rel. 40, Last annotation update)	
E C	a) i	precursor (EC 2.1.3.3)
4 2	(Olcase) (Ollithine ClaiscalDamylase).	
5 0	Rattus norvegious (Rat)	
8	data;	brata: Euteleostomi:
ဗ	a; Rodentia;	Sciurognathi; Muridae; Murinae; Rattus
×	NCBI_TaxID≈10116;	
R I		
괊;	SEQUENCE FROM N.A.	
X 6	MEDLINE*85063800; PubMed*6095294;	2
9 E	"Molecul M., Minia S., Moli M., Includin M., "Molecular cloning and purcleotide segmence of	And for rat ornithing
; <u>E</u>	carbamovitransferase precursor ".	ייייי דיייי
R.	Proc. Natl. Acad. Sci. U.S.A. 81:7412-7416(1984)	84).
RN		
КÞ	SEQUENCE FROM N.A.	
RC RC	STRAIN-Wistar; TISSUE-Liver;	
ΚX	MEDLINE-87317609; PubMed-3476935;	
R3	Takiguchi M., Murakami T., Miura S., Mori M.;	
RŢ	rat ornithin	sferase gene, a large,
RŢ	chromosome-linked gene with an atypical promoter."	
RI	c. Natl. Acad. Sci. U.S.A.	187).
RN I		
RP	SEQUENCE FROM N.A.	
X :		
<b>S</b>	С.Б.,	Horwich A.L., Kalousek F.,
RA	liams K.R., Rosenberg L.E.;	
£ 1	the precursor of r	ornithine
KT.	transcarbamylase: comparison of rat and human leader	leader sequences and
¥ ;	conservation of catalytic sites.";	
₹;	Nucleic Acids Res. 13:943-952(1985).	
Z		
<u>ب</u>	SEQUENCE FROM N.A.	
ž,	3350; PubMed=3838931;	
Z :	McIntyre P., Graf L., Mercer J.F.B., Wake S.A.,	, Hudson P.J.,
<b>5</b> 5		
9	iry structure or the import	ed mitochondrial protein,
2 6	amylase irom rat	NA Levels during
Z 2	ontogeny.";	
1 2	LE3	
2 0	[5] SECTIFINCE OF 33-56: 203-302: 307-317 AND 321-320	20
, <u>C</u>	ver.	
X	MEDITURE=88268748 · DubMed=3390141 ·	
Ø	Aoki Y., Sunada H., Suzuki K.T.:	
E	um-binding protein in rat liver	identified as ornithine
E	chamovltransferase.":	)
RL	Biochem, J. 250:735-742(1988).	

```
MEDLINE-87263407; PubMed-3603027;
Veres G., Gibbs R.A., Scherer S.E., Caskey C.T.;
"The molecular basis of the sparse fur mouse mutation.";
                                  Science 237:415-417(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ocnithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCASE) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                          TICRFAMS; TIGR00658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
+ L-citulline.
PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
SUBUNIT: HOMOCLIMEA.
SUBCELJULAR LOCATION: Mitochondrial matrix.
SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION.
ONNITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
C -> P (IN REF. 3; AAA41772).
G -> S (IN REF. 3).
W; 156B511AF7063F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 199; DB 1; Length 35
Pred. No. 9.2e-21;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                               Interpro; IPR006130; Asp/orn_cotranf.
Interpro; IPR002292; Orn_carbtransf.
Interpro; IPR006131; OrGace_O.
Interpro; IPR006132; OrGace_P.
Pfan; PF00185; OrGace, I.
Pfan; PF02729; OrGace, I.
                                                                                                                                                          M16933; AAA41769.1;
M16924; AAA41769.1;
M16925; AAA41769.1; JOINED.
M16926; AAA41769.1; JOINED.
M16929; AAA41769.1; JOINED.
M16939; AAA41769.1; JOINED.
M16930; AAA41769.1; JOINED.
M16932; AAA41769.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39886 MW;
                                                                                                                                                    EMBL; K03040; AAA41768.1; -.
                                                                                                                                                                                                                                                X01976; CAA26007.1; -. K00001; AAA41772.1; -. M11266; AAA41767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sh 91.7%;
L Similarity 97.6%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        263
303
304
241
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              PIR; A00563; OWRT
HSSP; P00480; 10Ti
InterPro; IPR0061
                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                          Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTC_MOUSE
P11725:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTC_MOUSE
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                     STRAIN-C57BL/6J;
MEDLINE-86524037; PubMed-3011788;
WEDLINE-86524037; PubMed-3011788;
Veres G., Craigen W.J., Caskey C.T.;
"The 5' flanking region of the ornithine transcarbamylase gene contains DNA sequences regulating tissue-specific expression.";
J. Biol. Chem. 261:7588-7591(1986).
-I- CATALXIIC ACTIVITX: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              TIGETAMS; TIGEO0658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLIFRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
Transit peptide. 32 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
               MEDLINE-88157717; PubMed-2831503;
Scherer S.E., Veres G., Caskey C.T.;
"The genetic structure of mouse ornithine transcarbamylase.";
Nucleic Acids Res. 16:1593-1601(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORNITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
H -> N (IN SPARSE FUR MOUSE).
G -> R (IN REF. 2).
33BBE5DIE98AA196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 164; DB 1; Le
Pred. No. 8.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR0066130; Asp/Orn_Cotranf.
InterPro; IPR002029; Orn_carbtransf.
InterPro; IPR006131; OrCace_O.
InterPro; IPR006132; OrCace_P.
Pfam; PF00185; OrCace_P.
Pfam; PF00185; OrCace_N:
PRINTS; PR00100; AOTCACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA39864.1; ALT_SEQ.
CAA30121.1; CAA30121.1; JOINED.
CAA30121.1; JOINED.
CAA30121.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 354
53 354
3 303
117
195
39765 MW; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A43609; OWMS.
HSSP; P00480; IOTH.
SWISS-2DPAGE; P11725; MOUSE.
MGD; MGI:97448; Otc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%;
llarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M17030; AAA39865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA30121.1;
CAA30121.1;
CAA30121.1;
CAA30121.1;
                                                                                                                    SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
303
117
195
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 35; Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X07098;
X07099;
X07100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M12716;
X07092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X07094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x07093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x07096;
```

 $\epsilon$ 

```
REAR SEE FEREN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20274073; PubMed-10813810; Shi D., Morizono H., Aoyagi M., Tuchman M., Allewell N.M.; Crystal structure of human ornithine transcarbamylase complexed with carbamoyl phosphate and L-norvaline at 1.9 A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horwich A.L., Fenton W.A., Williams K.R., Kalousek F., Kraus J.P., Doollittle R.F., Konigsberg W., Rosenberg L.B.;
"Structure and expression of a complementary DNA for the nuclear coded precursor of human mitochondrial ornithine transcarbamylase.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutations and polymorphisms in the human ornithine transcarbamylase
                                                                                                                                                                                                                                                                 precursor (EC 2.1.3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87057134; PubMed-3782067;
MEDLINE-87057134; PubMed-3782067;
Hata A., Tsuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda I.;
"Isolation and characterization of the human ornithine
"Iranscarbamylase gene: Structure of the 5'-end region.";
J. Blochem. 100:717-725(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99069419; PubMed-9652088;
Shi D., Morizono H., Ha Y., Aoyagi M., Tuchman M., Allewell N.M.;
I.85-A resolution crystal structure of human ornithine
transcarbamoylase complexed with N-phosphonacetyl-L-ornithine.
Catalytic mechanism and correlation with inherited deficiency.";
J. Biol. Chem. 273:34247-34254(1998).
                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88227905; PubMed-2836378; Hata A., Tsuzukt T., Shimada K., Takiguchi M., Mori M., Matsuda "Structure of the human ornithine transcarbamylase gene."; J. Biochem. 103:302-308(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85270440; PubMed-3895227;
HOTWICH A.L., Kalousek F., Rosenberg L.E.;
"Arginine in the leader peptide is required for both import and proteolytic cleavage of a mitochondrial precursor.";
Proc. Natl. Acad. Sci. U.S.A. 82:4930-4933(1985).
  MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                         21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
10-Tutthine carbamoyltransferase, mitochondrial)
(OrCase) (Ornithine transcarbamylase).
                                                                                                                                                        Æ
                                                                                                                                                      354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVIEW ON VARIANTS.
MEDLINE=93372868; PubMed=8364586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-84196410; PubMed~6372096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coded precursor of human mit
Science 224:1058-1074(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum. Mutat. 2:174-178(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbamoyl phosphate and L-Proteins 39:271-277(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-36 FROM N.A.
                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [8]
REVIEW ON VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuchman M.;
                                                                                                                                                    OTC_HUMAN
                                                                                                          RESULT 3
OTC_HUMAN
                                                                                                                                                        ò
                                       음
```

```
Gilbert-Dussardier B., Rabier D., Strautnieks S., Segues B., Bonnefont J.-P., Munnich A.; "A novel arginine (245) to glutamine change in exon 8 of the ornithine carbamoyl transferase gene in two unrelated children presenting with late onset deficiency and showing the same enzymatic pattern."; Hum. Mol. Genet. 3:831-832(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Patal hyperammonemia resulting from a C-to-T mutation at a MspI site of the ornithine transcarbamylase gene."; Hum. Genet. 88:153-156(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grompe M., Muzny D.M., Caskey C.T.; "Scanning detection of mutations in human ornithine transcarbamoylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          β
                              Tuchman M., Plante R.J.; "Mutations and polymorphisms in the human ornithine transcarbamylase gene: mutation update addendum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJINE-93126062; PubMed-1480464;
Tuchman M., Holzknecht R.A., Gueron A.B., Berry S.A., Tsai M.Y.;
Tichman M., mutations in the contintine transcarbamylase gene detected single-strand conformational polymorphism.";
Pediatr. Res. 32:600-604(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT OTCD GLN-141.
MEDLINE-89008892; PubMed=3170748;
Maddalena A., Spence J.E., O'Brien W.E., Nussbaum R.L.;
"Characterization of point mutations in the same arginine codon in three unrelated patients with ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90269805; PubMed-2347583;
Finkelstein J.E., Francomano C.A., Brusilow S.W., Traystman M.D.;
Vise of denaturing gradient gel electrophoresis for detection of
mutation and prospective diagnosis in late onset ornithine
transcarbamylase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93273296; PubMed-8099056; Tsai M.Y., Holzknecht R.A., Tuchman M.; Milderstrand conformational polymorphism and direct sequencing applied to carrier testing in families with ornithine transcarbamylase deficiency.";
                                                                                                                                                                                                                                                                        MEDLINE=96091868; PubMed-8544185; Tuchman M., Morizono H., Reish O., Yuan X., Allewell N.M.; Tuchman M., Morizono Gornithine transcarbamylase deficiency: modelling the human enzyme and the effects of mutations."; J. Med. Genet. 32:680-688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91118929; PubMed-1671317;
Grompe M., Caskey C.T., Fenvick R.G. Jr.;
"Improved molecular diagnostics for ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS OTCD GLN-26; PRO-45 AND GLU-216, AND VARIANT ARG-46 MEDLINE=89345570; Pubmed-2474822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT OTCD LEU-225.
MEDLINE-92098086; Pubmed-1721894;
Hentzen D., Pelet A., Feldman D., Rabier D., Berthelot J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 269-289 FROM N.A., AND VARIANT OTCD GLN-277.
MEDLINE-94362689; Pubmed-8081373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS OTCD GLN-92 AND LEU-320, AND VARIANT PRO-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS OTCD GLU-79; THR-94; PHE-304 AND ASP-345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 86:5888-5892(1989)
                                                                                                                                                                                                                                              ON VARIANTS, AND 3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am. J. Hum. Genet. 48:212-222(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Invest. 82:1353-1358(1988)
MEDLINE=95353279; PubMed=7627182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by chemical mismatch cleavage.
                                                                                                                                                       Hum. Mutat. 5:293-295(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 7:167-172(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WARIANT OTCD TRP-277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Munnich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deficiency
                                                                                                                                                                                                                                              REVIEW
```

597 AA

STANDARD;

IF2P\_METAC

/ARIANTS OTCD LEU-117; LEU-182 AND CYS-203.

Genet. 91:321-325(1993).

```
MEDLINE-94290509; PubMed-8019569; Tuchman M., Plante R.J., Giguere Y., Lemieux B.; Tuchman M., Plante R.J., Giguere Y., Lemieux B.; The constitution transcarbamylase gene: new 'private' mutations in four Hum. Mutat. 3:318-320(1994).
                                                                                                                                                                                                                                                       Sakaki Y., Matsuda I.; "Sanda I.; "Found I.; "Found I.; Matsuda I.; "Found I.; "Tour newly identified ornithine transcarbamylase (OTC) mutations (D126G, R129H, I172M and W332X) in Japanese male patients with early-onset OTC deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                             GIG-309 DEL.
MEDLINE-95038770; PubMed-7951259;
Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.;
Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.;
"Seven new mutations in the human ornithine transcarbamylase gene.";
Hum. Mutat. 4:57-60(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS OTCD MET-125, ARG-188; VAL-209 AND LEU-302.
MEDLINE-964(00964; PubMed-8807340;
Gilbert-bussardier B., Seques B., Rozet J.-M., Rabier D., Calvas P.
de Lumley L., Bonnefrod J.-P., Munnich A.;
"Partial duplication [dup. TCAC (178)] and novel point mutations
(T125M, G188R, ASO9Y, and H302L) of the ornithine transcarbamylase
Hum. Mutat. 8:74-76(1966).
                                                                                                                                                                           VARIANTS OTCD GLY-126; HIS-129 AND MET-172.
MEDLINE-94362715; PubMed-8081398;
Matsuura T., Hoshide R., Kiwaki K., Komaki S., Koike E., Endo F., Oyanagi K., Suzuki Y., Kato I., Ishikawa K., Yoda H., Kamitani S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A splicing mutation, a nonsense mutation (Y167X) and two missense mutations (I1597 and A208Y) in Spanish patients with ornithine transcarbamylase deficiency."; Hum. Genet. 96:549-551(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zimmer K.P., Matsuura T., Colombo J.-P., Koch H.G., Ullrich K., Deufel T., Harms E., Matsuda I.; A novel point mutation at codon 269 of the ornithine transcarbamylase (OTC) gene causing neonatal onset of OTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96070988; Pubmed=8530002;
Garcia-Perez M.A., Sanjurjo P., Briones P., Garcia-Munoz M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS OTCD HIS-40; ASN-88; TYR-202 AND ASN-263. Guardamagna O., Gatti E., Parini R., Plante R.J., Tuchman M.; "Genotype-phenotype correlations in ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                              VARIANTS OTCD HIS-40; HIS-129; ARG-195; THR-225; GLN-277 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS OTCD ASN-88; CYS-176; ALA-220; TYR-302 AND LYS-343.
MEDLINE-97114289; PubMed-8956038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.0%; Score 141; DB 1; Length 354; 69.0%; Pred. No. 1.7e-12; ive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                deficiency.";
J. Inherit. Metab. Dis. 18:356-357(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS OTCD THR-159 AND VAL-209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96086561; PubMed=7474905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzyme Protein 49:191-191(1996).
                                                                                                                                                                                                                                                                                                                                        Hum. Mutat. 3:402-406(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT OTCD GLU-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rubio V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
IF2P_METAC
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO Pubmed-1193238,

MEDINE-21929760;

Ralagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Ralagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Rallan N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Rayor J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Retcalf W.W., Birren B.;

The genome of Methanosarcina acetivorans reveals extensive metabolic

and physiological diversity.";

Genome Res. 12:532-542(2002).

1. FUNCTION: Function in general translation initiation by promoting

the binding of the formylmethiconine-tRNA to ribosomes. Seems to

function along with ferry SMMIIN;

C. -1. SIMILARITY: BELONGS TO THE IF-2 FAMIIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                              Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 1; Length 597; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R EMBL, AE010822; AAM04939.1; -.
R HANAP; MF_00100; -; 1.
INCLEPTO; IPR000795; EF_GTPDind.
R INCLEPTO; IPR000161; EFTU_D2.
R INCLEPTO; IPR000178; IE2.
R INCLEPTO; IPR00525; Small_GTP.
R INCLEPTO; IPR00525; Small_GTP.
R INCLEPTO; IPR00525; Small_GTP.
R PFam; PF000494; GTP_EFTU_D2.
R PFam; PF00314; GTP_EFTU_D2; 1.
R PFAm; PF00314; GTP_EFTU_D2; 1.
R TGRFAMS; TIGR00491; aIF-2; 1.
R TGRFAMS; TIGR00531; small_GTP, 1.
R PROSITE; PS01176; IF2; FALSE_NBG.
R INITIALION factor; Protein blosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 GTP (BY SIMILARITY).
88 GTP (BY SIMILARITY).
141 GTP (BY SIMILARITY).
65438 MW; 67CAP4D902CIBBD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ--LKPRDL 42
                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable translation initiation factor IF-2.
INFB OR MALS25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.3%;
Matches 14; Conservative 1:
                                                                                                                                           Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                   NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
IF2P_METMA
ID IF2P_METMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

Š

```
catesbeiana (Bull frog).
                                                                                                                                                                                             ISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RR2_LOTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=GOEJ / GOI / ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINE=2120827; PubMed=12125824;

AM BEDLINE=2120827; PubMed=12125824;

AM BEDLINE=2120827; PubMed=12.125824;

AM BEDLE T. Golden A., Hartech T., Merkl R., Schmitz R.A., Bratcher ann H., Lienard T., Christmann A., Boemecke M., Steckel S., Bratcherygamann H., Lienard T., Christmann A., Boemecke M., Steckel S., A Bratcherygamann H., Lightadis A., Overbeek R., Klenk H.-P., Gunsalus R.P., A Fritz H.-J., Gottschalk G.;

The genome of Methanosarchia mazei: evidence for lateral gene Transfer between Bacteria and Archaea H. 4453 461(2002).

The promortion of Methanosarchia and Archaea H. 433 461(2002).

The binding of the formylmethionine-tRNA to ribosomes. Seems to function along with FIF-2 FAMILY.

SEMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
                                                                                                                                                                                                                 Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.8%; Score 56; DB 1; Length 591; 33.3%; Pred. No. 3.7; Live 13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R EMBL; AE013490; AAM32159.1; -. R HAMAP; MF_00100; -: 1. InterPro; IPR000709; EF_GTPDind.
InterPro; IPR004161; EFTU_D2.
R InterPro; IPR004161; EFTU_D2.
R InterPro; IPR004255; SM31_GTP.
R InterPro; IPR004544; TIF_aTP-2.
R Ffam; PF00009; GTP_EFTU_1.
R Pfam; PF00009; GTP_EFTU_D2; I. R PR.MTS; PR000135; ELONGATURCT.
R TIGRPAMS; TIGR00491; aIF-2; 1. R TIGRPAMS; TIGR00491; aIF-2; R TIGRPAMS; TIGR00419; AIF-2; R TIGRDAMS; TIGR00419; AIF-2; TIGR00419; AIF-2; TIGR00419; AIF-2; TIGR0049; AIF-2; TIGR00419; AIF-2; TIGR0419; AIF-2; TIGR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 ATLDILLYDGTLKKGDTVVIGSL--GEPIRTKVRALLKPREL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
FE328265BBD887DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ--LKPRDL 42
                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
20-bable translation initiation factor IF-2.
INFB OR MM2463.
                                                                                                                                                                                    Methanosarcina mazei (Methanosarcina frisia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OTCase) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 82 G
132 135 G
591 AA; 64900 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 33.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=2209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTC_RANCA
P31326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTC_RANCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
STATEMENT NAMED DATA TO THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                      Helbing C., Gergely G., Atkinson B.G., "Sequential up-regulation of thyroid hormone beta receptor, ornithine transcarbamylase, and carbamyl phosphate synthetase mRNAs in the liver of Rana catesbelana tadpoles during spontaneous and thyroid hormone-induced metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
-!- SUBCULULAR LOCATION: Mitochondrial matrix.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- TISSUE SPECIFICITY: LIVER.
-!- PERCEDOMENTAL STAKE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
-!- INDUCTION: BY LIVICIDAL OF A DURING EMBRYONIC DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR06139; Asp/orn_Cotranf.
InterPro; IPR061292; Orn_carbtransf.
InterPro; IPR06131; OrCace_0.
InterPro; IPR06131; OrCace_0.
Figur, PF00183; OrCace_1.
Pfam; PF00183; OrCace_N: 1.
Pfam; PF00100; AOTCASE.
TIGRFAMS; TIGR00658; Orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOXILTRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
IWASS K., Yahmauchi K., Ishikawa K.;
IWASS K., Yahmauchi K., Ishikawa K.;
Wolecular cloning of bullfrog (Rana catesbelana) ornithine
transcarbamylase and induction of its mRNA during spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION (BY SIMILARITY).
ORNITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.3%; Score 55; DB 1; Length 350; 38.1%; Pred. No. 2.9; ive 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
E1E598355F03C13E CRC64;
                                                                                                                                                                             MEDLINE=93177976; PubMed=1291156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M95193; AAA49528.1; -.
EMBL; D38304; BAA22775.1; -.
PIR; A48421; A48421.
                                                                                                                                                                                                                                                                                                                                                          Dev. Genet. 13:289-301(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350
259
299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 25
299 25
350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00480; 10TH
                                                                                                                    SEQUENCE FROM N.A.
                                                        NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transit peptide.
```

ဖ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                       Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium, and Salmonella typhimurium, and Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacterialees; NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                         STRAIN-Accession MG-20; Mbmcd-11214967; MbDINE-21082929; PubMed-11214967; Rato T., Kaneko T., Sato S., Nakamura Y., Tabata S.; "Complete gtructure of the chloroplast genome of a legume, Lotus
                                                                                                                                                                                                                                                                                                                                                                                                                                 NA RES. 7:323-330(2000).
1-SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Oxygen-independent coproporphyrinogen III oxidase (EC 1....)
(COPTOPOTPHYTINOGENSE) (COPTOGEN OXIDASE).
HEMN OR STM4004 OR STY3877 OR T3617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 24.9%; Score 54; DB 1; Length 236; Local Similarity 38.5%; Pred. No. 2.6; les 10; Conservative 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-S.typhimurium; STRAIN-LT2;
MEDILINE-9425966; PubMed-8195073;
Xu K., Elliott T.;
"Cloning, DNA sequence, and complementation analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE9E238572325586 CRC64;
                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30s ribosomal protein S2.
  236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 IASIRLILNKLVFAICEGHSSYIRNF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; ME_00291; -; 1
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR005706; S2_bact_org.
Pfam; PF00318; Ribosomal_S2; 1.
PRINTS; PR00395; RIBOSOMAL_S2. 1.
IGRFAMS; TIGR01011; rpsB_bact; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LSNLRILLNKA--ALRKAHTSMVRNF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein; Chloroplast. SEQUENCE 236 AA; 26982 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002983; BAB33197.1; -. HAMAP; MF_00291; -; 1
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=34305;
                                                                                                                                                    Lotus japonicus.
                                                                                                                                                                           Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEMN SALTY
RR2_LOTJA
09BBS6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
HEMN_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        ONA
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARANA KARARA KAR
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-S.typhi; STRAIN-Ty2 / ATCC 700931; MEDLINE-22531367; PubMed-12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CI18.",
                                                                                                                                                                           SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed=11677609; MCDLINE-21534948; PubMed=11677609; MCDLINE-21534948; PubMed=11677609; MCDLINE-21534948; PubMed=11677609; Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PECIES-S. Typhi; STRAIN=CT18;
MEDLINE-21534947; PubMed=11677668;
MEDLINE-21534947; PubMed=11677668;
MEDLINE-21534947; PubMed=11677668;
MILLON Doughn G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungdal K.L., Benlley S.D., Holden M.T.G., Sebaliha M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Feltwell T., Hamilan N., Payles R.M., Dowd L., White N., Farrar J., Feltwell T., Hamilan N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Gonail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 54; DB 1; Length 457; 26.5%; Pred. No. 5.3; ive 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyrin biosynthesis; Oxidoreductase; Magnesium; NAD;
Complete proteome.
SEQUENCE 457 AA; 52828 MW; 5667B4FE76204DAB CRC64;
Salmonella typhimurium hemN gene encoding a putative oxygen-lidependent Coproporphiningen III oxidase."; J. Bacteriol. 176:3196-3203(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE00887; AAL22843.1; -...
EMBL; AL627280; CAD03096.1; -...
EMBL; AE016846; AAO71118.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF04055; Radical_SAM; 1.
SWART; SW00729; Elp3; 1.
TIGRFAMS; TIGR00538; hemN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U06779; AAA19690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        StyGene; SG10154; hemN.
InterPro; IPR006638; Elp3.
InterPro; IPR004558; HemN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                               SEQUENCE FROM N.A.
```

ó

ä

Gaps

2

Indels

15;

```
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36738 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y13045; CAA73480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 GKPVQSQVQLKPRDL
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328
237
277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 2
277 2
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                 OTC_PIG
019072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
  Matches
                                                                                                                                            RESULT 10
                                                                                                                                                                                                       ŏ
                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 728-1088 FROM N.A.
STRAIN-White leghborn; TISSUE-Embryonic retina;
MEDINES-94151328; PubMed=8108415;
Mang S.Z., Adler R.;
Adevelopmentally regulated basic-leucine zipper-like gene and its expression in embryonic retina and lens.";
Proc. Natl. Acad. Sci. U.S.A. 91:1351-1355(1994).
-: FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR STINDLE STABILIZATION: NUCLEAR, ASSOCIATED WITH MITOTIC
                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-White leghorn; TISSUE-Embryonic retina;
MEDLINE-95181533; PubMed-7876303;
Wang S.Z., Ahler R.;
Wang S.Z., Ahler R.;
Ghromokinesin: a DNA-binding, kinesin-like nuclear protein.";
J. Cell Biol. 128:761-768(1995).
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOMES.
-1- TISSUE SPECIFICITY: EXPRESSED IN PROLIFERATING CELLS;
NEUROEPITHELIUM OF EMBRYOS.
-1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CHROMOKINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1225; 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLED COIL (BY SIMILARITY). GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).

KG -> RI (IN REF. 2).

W; FA01ED83425F5875 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
MOTOR_PEOFEL; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR profein; Microtubules; APP-binding; DNA-binding; Nuclear protein; Coiled coil.
                                                                                                                                                       090640; 090608;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chromosome-associated kinesin KIF4A (Chromokinesin).
                     9 LNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                            PRT; 1225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINESIN-MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138923 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U18309; AAC59666.1; -. EMBL; U04821; AAA18960.1; -. PIR; A56514; A56514. HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%;
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1225
                                                                                                                                                                                                                                                                                                                                             Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
1087
                                                                                                                                          CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                    KF4A_CHICK
                                                                                                                                                              SOLUTION NO DEPARTMENT OF SOLUTION OF STREET STANDARD OF SOLUTION 
ò
                                      g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
0-nrithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + L-citrulline.
--- PATHWAT: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
---- SUBUNIT: HOMOTITHER (By similarity).
---- SUBCELLULAR LOCATION: Mitochondrial matrix.
----- SIMILARITY: BELONGS TO THE ATCASES/OFCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION (BY SIMILARITY). ORNITHINE CARBAMOYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.4%; Score 53; DB 1; Length 328; 66.7%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                             528 MSKELVELNKALALKEALAKKMIQNDSQLEPIQSQYQTNIKDL 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

BY SIMILARITY.

89302B9A471CD265 CRC64;
2 LSNLRILLNKA-ALRKA-HTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                      Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                   328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00480; 10TH.
InterPro; IPR006130; Asp/Orn_Cotranf.
InterPro; IPR005292; Orn_carbtransf.
InterPro; IPR006131; Offcace_O.
InterPro; IPR006132; Offcace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
MEDLINE-98080180; PubMed-9420013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
```

RESULT 11

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFP1_CHLMU
a
                                                                                                                                                                                                                                                                                                                                                                                        ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA MEDLINE-97313271; PubMed-9169875;

RA BUSSEY H., Storms R.K., Ahmed A., Albermann K., Alien E., Ansorge W., Araujo R., Aparidio A., Barrell B.G., Badcock K., Benes V., Araujo R., Araujo R., Araujo R., Carpenter J., Cherry J.M.,

RA BOTStein D., Bowman S., Barckner F., Davis R.W.,

RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

RA Hall J., Hebling U., Heumann K., Hibbert H., Hillier L.,

RA Hall J., Hebling U., Lashkarl D., Lew H., Lin A., Lin D., Louis E.J.,

RA Komp C., Kurdi O., Lashkarl D., Lew H., Lin A., Lin D., Louis E.J.,

RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

RA Marather S., Namath A., Nentwich U., Oefner P., Pearson D.,

RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Schrafen M.,

Scherens B., Schramm S., Schrades M., Sdicu A.M., Tetelin H.,

RA Scherens B., Schramm S., Voberndeer M., Sdicu A.M., Tetelin H.,

RA Abong W. W., Zollner A., Vob D.H., Hanl J.;

RT The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

RT The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

RA POSILIX FOR THE NORMAL PROGRESSION THROUGH MEIOSIS. INTERACTS

***THE PARTY THE NORMAL PROGRESSION THROUGH MEIOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      Epstein C.B., Cross F.R.;
"CLB5: a novel B cyclin from budding yeast with a role in S phase.";
Genes Dev. 6:1695-1706(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                      Schwob E., Nasmyth K.; "CLB5 and CLB6, a new pair of B cyclins involved in DNA replication in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·i - DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED JUST BEFORE CELL CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94074543; PubMed-8253070; Kuehne C., Linder P.; Ruehne C., Linder P.; A new pair of B-type cyclins from Saccharomyces cerevisiae that function early in the cell cycle."; EMBO J. 12:3437-3447(1993).
                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FBR-2003 (Rel. 41, Last annotation update)
S-phase entry cyclin 5.
CLBS OR YPR120C OR P9642.8
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceses; Saccharomyceses.
                 435 AA.
                 PRT;
                                                                                                                                                                                                                                                        STRAIN=BF264-15D;
MEDLINE=92387544; PubMed=1387626;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93307652; Pubmed-8319908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes Dev. 7:1160-1175(1993).
               STANDARD;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=4932;
             CGS5_YEAST
```

EMBL; M91209; AAA34503.1; -. EMBL; X70435; CAA49893.1; -.

```
between the Swiss Institute of Bloinformaties and the EMBL outstation—
the European Bloinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDGUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20150255; PubMed-10684935;
MEDLINE-20150255; PubMed-10684935;
Med T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pheumoniae AR39.";

Nucled Acids Res. 28.1397-1406(2000).

-I- FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT
TRANSLATION AND PEPTIDE BOND SYNTHESIS ON NATIVE OR RECONSTITUTED
TOS RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING
THEA REFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
THEAR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
(BY SIMILARITY).

-I- PATHWAY: PLOTEIN DIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
EMBL; U40828; AAB68061.1; -.

R PIR; 531290; 531290.
SGD; S0006324; CLB5.
GO; GO:00006824; CLB5.
R GO; GO:0000082; P:GJ/K transition of mitotic cell cycle; IEP.
GO; GO:0000085; P:GJ/K transition of mitotic cell cycle; IEP.
GO; GO:0000085; P:GJ/K transition of mitotic cell cycle; IEP.
R GO; GO:0000085; P:GJ/K transition of mitotic cell cycle; IEP.
R GO; GO:0000085; P:GJ/K transition of mitotic cell cycle; IEP.
R GO; GO:0006679; P:GJ/K CYCLIN.
R InterPro; IPR004867; CYCLIN.
R Pfam; PF02984; CYCLIN.
R PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 53; DB 1; Length 435; 46.4%; Pred. No. 7; Live 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                  Cyclin; Cell cycle; Cell division; Multigene family. SEQUENCE 435 AA; 50431 MW; 5AD67EB841BA5759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation factor P 1 (EF-P 1).
EFPI OR TC0398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SNLRILLNKAALRKAHTSMVRNFRYGKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 SNLKILQNKRALSKNDSSSKQQVQDSKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002306; AAF39255.1; -. PIR; B81708; B81708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00141; -; 1.
InterPro; IPR001059; EF-P.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; TC0398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFP1_CHLMU
Q9PKR6;
```

```
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-K12;
MEDLINE-97061202; Pubbed-8905232;
MEDLINE-97061202; Pubbed-8905232;
MEDLINE-97061202; Pubbed-8905232;
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampel G., Sekl Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=E.Col; STRAIN=K12;
MEDLINE=89263708; PubMed=2657652;
Mohno T., Noji S., Taniguchi S., Saito T.;
"The narX and narL genes encoding the nitrate-sensing regulators of Escherichia coll are homologous to a family of prokaryotic two-component regulatory genes."
Nucleic Acids Res. 17:2947-2957(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R. Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Navbew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Abantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                              Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                        ж
•
                                                             24.2%; Score 52.5; DB 1; Length 185;
larity 41.2%; Pred. No. 3.2;
Conservative 9; Mismatches 8; Indels
Pfam; PF01132; EFP; 1.
PROSITE; PS01275; EPP; 1.
Protein biosynthesis: Blongation factor: Complete proteome.
SEQUENCE 185 AA; 20468 MW; 969BD834F4997CE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-0157:H7 / EDL933 / AICC 700927;
MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                        01-071-1989 (Rel. 11, Created)
01-ANG-1992 (Rel. 23, Last sequence update)
01-ANG-1992 (Rel. 23, Last sequence update)
Nitrate/nitrite sensor protein narx (EC 2.7.3.-).
NARX OR NARR OR B1222 OR 21998 OR ECS1727 OR SF1225.
Escherichia coli, 0157:H7, and
                                                                                                              42
                                                                                                                            11 KAALRKAHISMV--RNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:529-533(2001).
                                                                                                                                                                                                    STANDARD;
                                                                         Local Similarity
les 14; Conserv
                                                                                                                                                                                                NARX_ECOLI
P10956;
                                                              Query Match
                                                                            Best Loc
Matches
                                                                                                              ŏ
                                                                                                                                      g
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MANION C. G., Ohtsubo E., Nakama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4422-4441(2002).

-1- FUNCTION: ACTS AS A SENSOR FOR NITRATE NITRITE AND TRANSDUCES SIGNAL OF NITRATE AVAILABLILITY TO THE NARL PROTEIN AND OF BOTH NITRATE TO THE NARP PROTEIN NARX PROBABLY ACTIVATES NARL AND NARP BY PHOSPHORYLATION IN THE PRESENCE OF NITRATE. NARX ALSO PLAXS A NEGATIVE ROLE IN CONTROLLING NARL ACTIVITY, PROBABLY THROUGH DEPHOSPHORYLATION IN THE ABSENCE OF NITRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-E.coli; STRAIN=K12;
MEDLINE=89338707: PubMed=2668029;
Noji S., Mohno T., Salto T., Taniguchi S.;
The narK gene product participates in nitrate transport induced in
Escherichia coli nitrate-respiring cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-E_coli; STRAIN-K12;
MEDDINE-69197802; PubMed-2649492;
Stewart V., Parales J. Jr., Merkel S.M.;
"Structure of genes narL and narX of the nar (nitrate reductase)
locus in Escherichia coli K.12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-60 FROM N.A.
SPECIES-E.coli, STRAIN-K12 / MC4100;
Cavicchioli R., Gunsalus R.P., Chiang R.C.;
Submitted (40G-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Probable).
--- SIMILARITY: Contains 1 HAMP domain.
--- SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol, 171:2229-2234(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE000220; AAC74306.1; -. D90757; BAA36090.1; -. AE005339; AAG56082.1; -. AP002556; BAB35150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X13360; CAA31741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 56-598 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE015149; AAN42838.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X15996; CAA34125.1;
M24910; AAA24198.1;
X65715; CAA46631.1;
X69189; CAA48934.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-55 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
```

```
506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HISTIDINE KINASE.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
GSAHAINKAGS -> AAPMRSTKRDA (IN REF. 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21668955; PubMed=11809834; Katayama S., Kitamura K., Lehmann A., Nikaido O., Toda T.; Fitsaton yeast F-box protein Pof3 is required for genome integrity and telomere function...; Mol. Biol. Cell 13:211-224(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourco J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Barooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Helrotyd S., Hornsby T., Howards S., Hockle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
;;
                                                                                                                                                                                                                                                                                       SMART; SM00304; HAMP; I.
SMART; SM00387; HAPPase_c; 1.
SMART; SM00388; HisKA; 1.
PROSITE; PS50889; HISKA; 1.
PROSITE; PS50809; HIS_KIN; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Nitrate assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.0%; Score 52; DB 1; Length 598; Best Local Similarity 31.0%; Pred. No. 14; Matches 13; Conservative 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 LLTTFRLOLTEPGLRPALEASCEEYSAKFGFPVKLDYQLPPR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLSNLRILLNKAALRKAHTSMVRNF--RYGKPVQSQVQLKPR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> G (IN REF. 7).
886BA0FC2C8F3C3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POFB_SCHPO
09885; 09P7V1;
001885; 09P7V1;
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
P.Dox/MD-repeat protein pof11.
F.Dox/MD-repeat pof11.
F.Dox/MD-repeat protein pof11.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
PIR; F85702; F85702.
PIR; G90844; G90844.
PIR; S526137; RECNX.
ECGGene; EG10646; narx.
InterPro; IPR003594; Arbbind_ArPase.
InterPro; IPR003661; His_kinA.
InterPro; IPR003661; His_kinA.
InterPro; IPR003661; His_kinA.
Pfam; PF00572; HAMP; 1.
Pfam; PF00572; HAMP; 1.
Pram; PF00572; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67083 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
37
151
174
174
598
399
399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
POFB_SCHPO
         DRA DORAN DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Askelton J., Simmonds M., Squares R., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Melish I., Vanstreels E., Rabben J., Grymonprez B., Melish I., Vanstreels E., Raper M., Schaefer M., Meller-Auer S., Abelis I., Vanstreels E., Horger M., Schaefer M., Meller-Huer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., A Borzym K., Langer I., Beck A., Lehrach H., Rinhardt R., Pohl T.M., AB Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galbert F., Aves S.J., Xiang Z., Hunt C., More K., Hurst S.M., Rochet M., Gaillardin C., Pallada V.A., Garzon A., Thode G. Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Aboniquez A., Revuelta J.L., Moreno S., Ammstrong J., Porsburg S.L., Abhakovski G.V., Ussery D., Barrell B.G., Nurse P., The Genome sequence of Schizosaccharomyces pombe.";

Mature 415:871-880(2002)

C. I. SIMILARITY: Contains 1 F-box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.5%; Score 51; DB 1; Length 506; Best Local Similarity 44.4%; Pred. No. 16; Matches 12; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEF34D4EFFBC2E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     705 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 35, Created)
(Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 SNGRPLLNWSYLYKEHAHLDSNWRHGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SNLRILLNKAALRKAHTSMVRNFRYGK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB061694; BAB55543.1; -. EMBL; AL136538; CAB66464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58257 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
YM37_YEAST
ID YM37_YEAST
AC Q03824;
DT 01-NOV-1997 (
DT 01-NOV-1997 (
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                      Bowman S., Chircher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
                                                                 Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 81.5 kDa protein in HLJ1-SMP2 intergenic region.
YMR163C OR YM8520.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.5%; Score 51; DB 1; Length 705; Best Local Similarity 36.8%; Pred. No. 23; Matches 14; Conservative 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z49705; CAA89799.1; -.
PIR; S54521; S54521.
SGD; S000473; YMR13C.
Hypothetical protein.
SEQUENCE 705 AA; 81466 MW; E4F2A4D205A98F66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 LRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                     Nature 387:90-93(1997).
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288c / AB972;
PubMed-9169872;
      δŽ
```

Search completed: July 24, 2003, 22:04:32 Job time: 8.67857 secs

|| : |||| || || || 643 LRTAKSFELLRKAQASMSVKFGFQKPLRDDAFLESRPL 680

g

\_

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

del
щoф
S
using
search,
protein
1
protein
Ö

Run on:

July 24, 2003, 22:02:24; Search time 14.3333 Seconds (without alignments) 288.506 Million cell updates/sec

US-08-765-244-22 217 1 MLSNLRILLNKAALRKAHTS.....NFRYGKFVQSQVQLKPRDLC 43 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	ornithine carbamoy	ornithine carbamoy	ornithine carbamoy	ornithine transcar	hypothetical prote	7)	ornithine carbamoy	F16F4.13 protein -	ornithine transcar	hypothetical prote	oxygen-independent	chromokinesin - ch	sensor-like protei	cyclin B5 - yeast	nitrate/nitrite se	nitrate/nitrite se	translation elonga	probable two-compo	hypothetical prote	nitrate/nitrite se	nitrate/nitrite se	nitrate/nitrite se	hypothetical prote	WD-repeat protein	nitrate/nitrite se	hypothetical prote		hypothetical prote	hypothetical prote
SUMMAKIES	QI	OWRT	OWINS	OWHU	I52779	B71413	F90409	JE0309	A86345	A48421	T32702	AD0950	A56514	I40646	S31290	T47000	AB0239	B81708	B83182	T33457	RGECNX	F85702	G90844	G70233	T50211	AF0648	S76749	S54521	m	ထ
	DB	-	Н	Н	~	7	7	7	7	7	7	7	7	ď	N	~	~	~	7	7	-	N	7	N	~	N	ď	N	7	Ġ
	Length	354	354	354	41	1286	351	354	454	350	300	457	1225	425	435	293	593	185	213	335	598	598	298	260	206	598	633	705	1779	138
dЯ	Query	91.7	S	S	54.8	ω	7	9	S	വ	4	4	4	4	4	24.4	4	4	4	4	4	4	4	ന	ന	m	23.5	ന	m	m
	Score		9	141	$\vdash$	61	9	S	55.5	55	54	54	54	53.5	53	53	53	52.5	52	52	52	52	52	51.5	51	51	51	51	51	50.5
	Result No.	-	7	m	4	S	9	7	œ	σ	. 10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

short-chain-specif hypothetical prote hypothetical prote	hypothetical prote moth homolog lafu CAAX prenyl protei probable molybdopt signal recognition	calcium-dependent cytochrome c PA303 purine NTPase [imp tumor suppressor p 18c protein (clone	hypothetical prote GTP-binding protei conserved hypothet
B83922 E90267 F91180	H86026 F40590 F72773 A58947	AB1979 683266 B90395 T03814 S57240	T33068 B69518 C81719
000	00000	ичйичи	1212
383 429 178	178 202 338 386 616	662 467 864 1164	301 355 446
mmo	00000	0 0 0 0 0	999
233.	23.000.000.0000.00000000000000000000000	22223	555
50.5 50.5 50	00000 00000	449.50 449.55 49.55	4 4 4 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
30 31 32	2 2 2 2 2 2 3 2 4 3 3 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5	8 8 8 4 4 4 8 0 0 1 C	444

# ALIGNMENTS

	RESULT 1  OWRT  ornithine carbamoyltransferase (EC 2.1.3.3) precursor - rat  ornithine carbamoyltransferase (EC 2.1.3.3) precursor - rat  ornithine carbamoyltransferase (EC 2.1.3.3) precursor - rat  NAlternate names: citruiline phosphorylase; ornithine transcarbamylase C; Species: Rattus norvegicus (Norvay rat; C; Species: Re-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 11-Jun-1999 C; Accession: A00563; A28042; A23090; S02466; I52976; I67609; I53457 R; Takiguchi, M.; Muura, S.; Mori, M.; Tatibana, M.; Nagata, S.; Kaziro, Y. Proc. Natl. Acad. Sci. U.SA. 81, 71127416, 1984 A; Title: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamo; A; Reference number: A00563; MUID: 85063800; PMID: 6095294
· · · · · · · · · · · · · · · · · · ·	A; Molecule type: mRNA A; Residues: 1-354 «TRXI> A; Cross-references: GB:K03040; NID:g205873; PIDN:AAA41768.1; PID:g205874 A; Cross-references: GB:K03040; NID:g205873; PIDN:AAA41768.1; PID:g205874 R; Takiguchi, M.; Murakami, T.; Miura, S.; Mori, M. Proc. Natl. Acad. Sci. U.S.A. 84, 6136-6140; 1987 A; Title: Structure of the rat ornithine carbamoyitransferase gene, a large, X chromos A; Reference number: A28042; MUID:87317609; PMID:3476935
	A; Residues: 1-354 CTAR(2) A; Residues: 1-354 CTAR(2) A; Cross-references: GB:M16933; GB:J02957; NID:g205884; PIDN:AAA41769.1; PID:g205886 A; Cross-references: GB:M16933; GB:J02957; NID:g205884; PIDN:AAA41769.1; PID:g205886 R; Kraus, J.P.; Hodges, P.E.; Williamson, C.L.; Horwich, A.L.; Kalousek, F.; Williams, Nucleic Acids Res. 13, 943-952, 1985 A; Title: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamyle A; Reference number: A23090; MUD:85215524; PMID:3839075 A; Reseasion: A23090 A; Molecule type: mRNA A; Residues: 1-38, 'P', 40-240, 'S', 242-354 <kra></kra>
	A;Cross-references: GB:X01976 R;Aoki, Y.; Sunaga, H.; Suzuki, K.T. B;Aoki, Y.; Sunaga, H.; Suzuki, K.T. B;Aoki, Y.; Sunaga, H.; Suzuki, K.T. B;Aoki, Y.; Sunaga, H.; Suzuki, K.T. B;Achille: A cadmium-binding protein in rat liver identified as ornithine carbamoyltrar A;Reference number: S02466; MUID:88268748; PMID:3390141 A;Reference number: S02466 A;Molecule type: protein A;Residues: 33-56;293-302;307-317;322-329 CAOK> B;Residues: 33-56;293-302;307-317;322-329 CAOK> R;McIntyre, P.; Graf, L.; Mercer, J.F.B.; Wake, S.A.; Hudson, P.J.; Hoogenraad, N.
	DNA 4, 147-155, 1985  A;Title: The primary structure of the imported mitochondrial protein, ornithine trans A;Title: The primary structure of the imported mitochondrial protein, ornithine trans A;Reference number: 152976; MUID:85203360; PMID:3838931  A;Reference number: 152976; MUID:85203360; PMID:3838931  A;Rotus: translated from GB/EMBL/DDBJ  A;Status: translated from GB/EMBL/DDBJ  A;Rotus: translated from GB/EMBL/DDBJ  A;Rotus: translated from GB/EMBL/DDBJ  A;Rotus: translated from GB/EMBL/DDBJ  A;Rotus: 1.354 & RES>  R;MCINCYTE, P: Graf, L: Mercer, J: Peterson, G: Hudson, P.J: Hoogenraad, N. FEBS Lett. 177, 41-46, 1984  A;Title: A highly basic N-terminal extension of the mitochondrial matrix enzyme ornit A;Reference number: 153457; MUID:85051832; PMID:6548714

~

ö

```
A; Molecule type: MRNA
A; Residues: 1.354 (ARA2)
A; Cravich, A.L.; Fenton, W.A.; Williams, K.R.; Kalousek, F.; Kraus, J.P.; Doolittle, Science 224, 1068-1074, 1984
A; Title: Structure and expression of a complementary DNA for the nuclear coded precur A; Reference number: A00562; MUID:84196410; PMID:6372096
A; Accession: A00562; MUID:84196410; PMID:6372096
A; Accession: A00562
A; Molecule type: mRNA
A; Residues: 1-100, Fr', 102-110, P', 112-192, CF', 195-269, R', 271-354 <HOR>
A; Cross-references: GB:D00230
A; Molecule type: mRNA
A; Residues: 1-100, 77-725, 1986
A; Title: Isolation and characterization of the human ornithine transcarbamylase gene: A; Reference number: 138078
A; Title: Isolation not shown
A; Residues: 1-26 <RES
A; Cross-references: EMBL:X04443; NID:935162; PIDN:CAA28039-1; PID:935163
A; Cooss-references: EMBL:X04443; NID:935162; PIDN:CAA28039-1; PID:935163
B; Wheeler V.C.; Prodromou, C.P.; Pearl, L.H.; Williamson, R.; Coutelle, C. Gene 169, 251-255, 1996
A; Title: Synthesis of a modified gene encoding human ornithine transcarbamylase for e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:M11235; NID:q189408; PIDN:AAA59976.1; PID:q189409
A;Cross-references: GB:M11235; NID:q189408; PIDN:AAA59976.1; PID:q189409
B;Gilbert-Dussardier, B.; Rabler, D.; Strautnieks, S.; Seques, B.; Bonnefont, J.P.; M
Hum. Mol. Genet. 3, 831-832, 1994
A;Title: A novel arginine (245) to glutamine change in exon 8 of the ornithine carbam
C pattern.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 269-276, 'Q',278-289 <RE3>
A; Cross-references: GB:573640; NID:9688001; PIDN:AB31859.1; PID:9688002
A; Cross-references: GB:573640; NIG:9688001; PIDN:AB31859.1; PID:9688002
A; Cross-references: GB:573640; NIG:9688001; PIDN:AB31859.1; PID:9688002
C; Comment: This sequence represents a disease defect in ornithine carbamoyltransferase
C; Comment: The active enzyme is a dimer of identical chains with one tightly bound zi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     both import and proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
A, Residues: 'M', 33-100, F', 102-110, 'P', 112-192, 'CF', 195-269, 'R', 271-354 < WHE>
A, Note: this report represents a synthetic gene designed for expression in (rather
R, Horwich, A.L.; Kalousek, F.; Rosenberg, L.E.
Proc. Natl. Acad. Sci. U.S.A. 82, 4930-4933, 1985
A, Title: Arginine in the leader peptide is required for both import and proteolytic
A, Reference number: 159039, MUID:85270440; PMID:3895227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross_references: GB:D00230; NID:g219957; PIDN:BAA00161.1; PID:g219959
A;Accession: B41444
                                                                                                                                                                                                                                                                                                                                                                                                          ornithine carbamoyltransferase (EC 2.1.3.3) precursor - human N.Alternate names: citrulline phosphorylase; ornithine transcarbamylase
                               ó
                                   Indels
                                                                                                                                                             1 MESNLRILINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL
                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: JC4672; MJID:96194812; PMID:8647457
A; Accession: JC4672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: 154377; MUID: 94362689; PMID: 8081373
                               5.
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: 154377
A; Status: translated from GB/EMBL/DDBJ
                               5;
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A41444
A; Molecule type: DNA
A; Residues: 1-354 <HAT>
                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enetic defect.
                               Matches
                                                                                                                õ
                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OWING

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-102 cRE2>
A;Cross-references: EMBL:X01178; NID:956802; PIDN:CAA25618.1; PID:956803
A;Accession: 153457
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-43, 'N', 45-99; 'R', 101-102 cRE3>
A;Cross-references: GB:K03041; NID:9205889; PIDN:AA41771.1; PID:9205890
C;Genetics: A;Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
A;Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
C;Gywords: arginine blosynthesis; homotrimer; mitochondino; transferase; urea cycle
F;1-32/Domain: transit peptide (mitochondrion) #status predicted cYNP>
F;33-354/Product: ornithine carbamoyltransferase #status predicted cYNP>
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology cACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: orbithine carbamoyltransferase; aspartate/orbithine carbamoyltransferase C;Keywords: mitochondrion; transferase; urea cycle F;1-32/Domain: transit peptide (mitochondrion) #status predicted <TMP> F;3-33/Product: orbithine carbamoyltransferase #status predicted <MAT> F;40-342/Domain: aspartate/orbithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 164; DB 1; Length 354; Pred. No. 6.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
91.7%; Score 199; DB 1;
Best Local Similarity 97.6%; Pred. No. 9.3e-20;
Matches 41; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.6%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
```

RESULT 2

δ g ቲ

us-08-765-244-22.rpr

ô

Gaps

```
Greenes: Sulfolobus solfatarious
C; Species: Sulfolobus solfatarious
C; Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C; Accession: F90409
R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; C; Jong, L.; Jeffities, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Thi-Ngoc, H.P.; Redder submitted to GenBank, April 2001
A; Reference number: A99139
A; Accession: F90409
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-351 < KURP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ornithine carbamoyltransferase (BC 2.1.3.3) - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C;Accession: JE0309
R;Shimogiri, T.; Kono, M.; Mannen, H.; Mizutani, M.; Tsuji, S.
J; Blochem. 124, 962-971, 1988
A;Title: Chicken ornithine transcarbamylase gene, structure, regulation, and chromosc A;Reference number: JE0309; MUID:99011321; PMID:9792920
A;Accession: JE0309
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:AF065629; NID:94218928; PIDN:AAD12234.1; PID:94218929
C,Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransfera
C,Keywords: transferase
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology <AOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C;Accession: A86345
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE006641; NID:g13815687; PIDN:AAK42533.1; GSPDB:GN00155 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 2; Length 354
Pred. No. 4.5;
4; Mismatches 21; Indels
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ILLINKAA-----IRKAHTSMVRNFRY----GKPVQSQVQ-
                                                                                                                                                                                                                  107 SNERWESSSTTKRDESLVRNLLLVSPIQLDIQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60; DB 2;
Pred. No. 1.7;
8; Mismatches 10
                                                                                                                                          3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ
                      Pred. No. 5.2;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F16F4.13 protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.3%;
Best Local Similarity 40.5%;
Matches 17; Conservative
                      38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.6%;
Best Local Similarity 34.6%;
Matches 18; Conservative
                 Best Local Similarity 38.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-354 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
A86345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                               ö
                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein d13525w - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)

A;Vartety: columbia (mouse-ear cress)

A;Vartety: columbia (mouse-ear cress)

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000

C;Accession: B71413

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk

P.; Wedler, H.; Wedler, E.; Wanbutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans

c.; Chalwatzis, N.

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Recession: B71413

A;Accession: B71413

A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ornithine transcarbamylase peptide - rat (fragment)
C.Specides: Rattus sp. (rat)
C.Specides: Rattus sp. (rat)
C.Specides: 152779
E.Rattus sp. (rat)
C.Accesion: 152779
C.Ratousek, F.; Fenton, W.A.; Pollock, R.A.; Rosenberg, L.E.
Cell 44, 451-459, 1986
A.Fitte: Targeting of pre-ornithine transcarbamylase to mitochondria: Definition of critt A.Reference number: 152779; MUID:86106223; PMID:3943133
A.Reference number: 152779; MUID:86106223; PMID:3943133
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-41 - RES
A.Residues: 1-41 - RES
A.Residues: 1-41 - RES
A.Cross-references: GB-MI2583; NID:9205887; PIDN:AAA41770.1; PID:9205888
C.Superfamily: ornithine carbamoyltransferase
                                                                   ornit
synthesis of UMP. Comment: The active enzyme catalyzes the condensation of carbamoyl phosphate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Map position: 4COP9-4G3845
Superfamily: Arabidopsis thaliana hypothetical protein dl3525w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 119; DB 2; L
Pred. No. 1.1e-09;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ë,

Gaps

ö

ö

Gaps

```
Oxygen-independent coproporphyrinogen III oxidase [imported] - Salmonella enterica su CiSpecies: Salmonella enterica subsp. enterica serovar Typhi CiSpecies: Salmonella enterica subsp. enterica serovar Typhi CiSpecies: Salmonella tryphi CiSpecies: Salmonella tryphi CiDate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 Righarkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr S.; Moule, S.; O'Gaora, P.
Alathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-457 CARP>
A; Cross-references: GB:AL513382; PIDN:CAD03096.1; PID:g16504733; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Nacession: Argust
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1225 < WANN
A; Cross-references: GB:U18309; NID:g603760; PIDN:AAC59666.1; PID:g603761
B; Wang, S.Z.; Adder, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 1351-1355, 1894
A; Title: A developmentally regulated basic-leucine zipper-like gene and its expression
A; Reference number: A33451; MUD:94181328; PMID:8108415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromokinesin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-7ul-1995 #sequence_revision 28-Jul-1995 #text_change 02-Feb-2001
C;Accession: A56514; I50691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 728-1086,'RI' <WA2>
A; Cross-references: EMBL:U04821; NID:g440792; PIDN:AAA18960.1; PID:g440793
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Wang, S.Z.; Adler, R.
J. Cell Biol. 128, 761-768, 1995
A;Title: Chromokinesin: a DNA-binding, kinesin-like nuclear protein.
A;Reference number: A56514; MUID:95181533; PMID:7876303
A;Accession: A56514
                                                                    A Gene: CESP:C14C6.13
A;Map position: 5
A:Introns: 91.1, 129/2; 145/3; 267/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.13
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                Ouery Match 24.9%; Score 54; DB 2; Length 300; Best Local Similarity 31.4%; Pred. No. 9.9; Matches 11; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: STY3877
C;Superfamily: oxygen-independent coproporphyrinogen oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.9%; Score 54; DB 2; Le Best Local Similarity 26.5%; Pred. No. 16; Matches 9; Conservative 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 LDNIRELCGOSALOKCSETRDPNTGFYRPINSELO 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: sw3-3
                               C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Action of the transcarbamylase - builfrog confithine transcarbamylase - builfrog confithine transcarbamylase - builfrog confithine transcarbamylase - builfrog confithine transcarbamylase confithine transcarbamylase confithine transcarbamylase sales and category confithine transcarbamylase confithing, C.; Genet. 13, 289-301, 1992

R; Helbung, C.; Genet. 13, 289-301, 1992

R; Helbung, C.; Genet. 13, 289-301, 1992

A; Title: Sequential up-regulation of thyroid hormone beta receptor, ornithine transcarbamylariod hormone-induced metamorphosis.

A; Reference number: A48421; MuID:93177976; PMID:1291156

A; Actual: preliminary

A; Molecule type: nucleic acid

A; Reperimental source: 11ver

A; Reperimental source: 11ver

A; Experimental source
ansen, N.F.; Hughes, B.; Huizar, L.
Atture 408, 816.810, 200.
Atture 50.
Atture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C14C6.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000 C;Accession: T32702

R;David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B. Submitted to the EMBL Data Library, December 1997

A;Reference number: 221210

A;Reference number: 221210

A;Accession: T32702

A;Accession: T32702

A;Accession: T32702

A;Molecule type: DNA

A;Residues: 1-300 < DAV>
A;Residues: 1-300 < DAV>
A;Cross-references: EMBL:AF039051; PIDN:AAB94269.1; GSPDB:GN00023; CESP:C14C6.13
A;Experimental source: strain Bristol N2; clone C14C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 25.3%; Score 55; DB 2; Length 350; Best Local Similarity 38.1%; Pred. No. 8.5; Matches 16; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.5; DB 2;
Pred. No. 9.6;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| : | | || : || || : || || || 422 KAAYSRISTDSPSRNYRESQPMGSPVQARPR 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 KAALRKAHT-SMVRNFRYGKPVQSQVQLKPR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.6%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

ö

ó

Gaps

```
R;Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carr submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: 224348
A;Accession: T47000
                                          A; Molecule type: DNA
A; Residues: 1-435 < JOH>
A; Residues: 1-435 < JOH>
A; Residues: 1-435 < JOH>
A; Construction: EMBL: U40828; NID: 91066467; PIDN: AAB68061.1; PID: 91066475; MIPS: Yi
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: CLB5
A; Cross-references: SGD: S0006324
A; Map Position: 16R
C; Superfamily: cyclin
C; Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain 6/69
C; Superfamily: nitrate/hittite sensor protein narX
C; Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase
F; 401/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitrate/nitrite sensor protein (BC 2.7.3.-) [similarity] - Yersinia pestis C; Species: Yersinia pestis C; Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000 C; Accession: T47000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 435;
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 LLTTFRLKLNEATLEAALQALVNEFSERAGLSITFKYQLPP 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLSNLRILLINKAALRKAHTSMVRNF--RYGKPVQSQVQLKP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-593 - 400C> A; Residues: 1-593 - 40C> A; Cross-references: EMBL:AL031866; PIDN:CAA21343.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.4%; Score 53; DB 2
Best Local Similarity 34.1%; Pred. No. 29;
Matches 14; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 SNLKILQNKRALSKNDSSSKQQVQDSKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SNLRILLNKAALRKAHTSMVRNFRYGKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: July 24, 2003, 22:08:08 Job time: 16.3333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.4%;
Best Local Similarity 46.4%;
Matches 13; Conservative
    A; Accession: S69013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-435 < CEPS.
A; Residues: 1-435 < CEPS.
A; Creating Since Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             As Gene: grsA
C; Superfamily: env2 protein; sensor histidine kinase homology
C; Superfamily: env2 protein; phosphohistidine; phosphoprotein
C; Keywords: autophosphorylation; phosphohistidine; phosphorylation) #status predicte
F; 196-421/Domain: sensor histidine kinase homology <SHK>
F; 227/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicte
C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology Keywords APP. DNA binding; mitosis; nucleotide binding; P-Loop F:11-344/Domain: kinesin motor domain Momology < KMOT> F:88-95/Region: nucleotide-binding motif A (P-Loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Coxiella burnetii
C; Species: Coxiella burnetii
C; Species: Coxiella burnetii
C; Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 31-Mar-2000
C; Accession: 140646
R; Mo, Yr Y. Mallaria, L.P.
Gene 151, 185-190, 1994
A; Title: A coxiella burnetii gene encodes a sensor-like protein.
A; Reference number: 140646; MUID: 95129857; PMID: 7828872
A; Reference number: 140646
A; Scatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1425 < RES>
C; Genetics:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclin B5 - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein P9642.8; protein YPR120c
Cispecies: Saccharomyces cerevisiae
Cispecies: Saccharomyces cerevisiae
Cispecies: Saccharomyces cerevisiae
Cispecies: 28-May-1993 #sequence_revision 28-May-1993 #text_change 19-Apr-2002
Cispecies: S1290; S362298; S69013
Ripperein, C.B.; Cross, F.R.
Genes Dev. 6, 1695-1706, 1992
A;Thle: CLBS: a novel B cyclin from budding yeast with a role in S phase.
A;Reference number: S31290; MUID:92387544; PMID:1387626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL:X70435; NID:g396496; PIDN:CAA49893.1; PID:g396497 R; Johnson, D. submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                       ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 425;
                                                                                                                                                                                                                    Score 54; DB 2; Length 1225;
Pred. No. 46;
9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Match 24.7%; Score 53.5; DB 2; Length 4 Local Similarity 36.4%; Pred. No. 17; hes 12; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSNLRILLNKA-ALRKA-HTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: The sequence of S. cerevisiae cosmid 9642 A;Reference number: S69014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 IKILGRASALKRAFINLLNNAIRYAKNVNVRIQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LRILLNKAALRKAHTSMVRN-FRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-435 <SCH>
                                                                                                                                                                                                                         Query Match 24.9%;
Best Local Similarity 39.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

ä

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

July 24, 2003, 21:59:18; Search time 37.881 Seconds (without alignments) 180.176 Million cell updates/sec 217 1 MLSNLRILLINKAALRKAHTS.....NFRYGKPVQSQVQLKPRDLC 43 OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-765-244-22 Perfect score: Scoring table: Sequence: Run on: Title:

1107863 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

length: 0 length: 2000000000 DB sed DB sed Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

: SIDSI/goddata/geneseq/geneseqp-embl/AA1980.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1984.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1985.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1987.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1989.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1989.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1980.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1991.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1991.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1993.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1992.DAT:\*
: SIDSI/goddata/geneseq/geneseqp-embl/AA1995.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\* /SIDS1/gcgdata/geneseq/genesegp-emb1/AA1996. /SIDS1/gcgdata/geneseg/genesegp-emb1/AA1997. A\_Geneseq\_19Jun03:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Rat ornithine tran	Rat ornithine tran	Protein encoded by	Human ornithine tr	OTC peptide fragme	Mitochondrial matr	Mitochondrial matr	Localisation seque	Mitochondrial matr
	OT.	AAR90584	ABG30857	AAB18445	ABG30856	AAG64224	AAR48260	AAW96358	ABG92993	ABP56588
į	: :	17	23	21	23	22	15	20	23	24
% Query	Length	43	32	258	32	32	32	32	32	32
Query	Match	100.0	73.3	50.2	49.8	48.4	42.4	42.4	42.4	42.4
	score	217	159	109	108	105	92	92	92	8
Result	. ON .	т	7	m	4	Ŋ	9	7	œ	on.

Replicable and transcriptionally active plasmid carrying signal peptide for specific target - useful for site directed mutagenesis

ondrial ondrial ondrial ondrial ondrial ondrial ondrial mila me cretium mila me ria mer ria me	Protein involved i Enterococcus faeca Enterococcus faeca C glutamicum prote Protein encoded by Rianodin receptor. MH mutant porcine Ryanodine receptor Novel human diagno Human ryanodine re Peptide Ms - 34, wit Human transferrin Human secreted pro
21 AAB15704 22 AAB22835 22 AAB22468 22 AAB22468 22 AAB57441 22 AAB57241 22 AAB57241 22 AAB671466 23 AAB671466 23 AAB67140 23 AAB77140 23 AAB77140 23 AAB77140 23 AAB77140 24 AAB77140 25 AAB77140 25 AAB77140 26 AAB77140 27 AAB77140 28 AAB77140 28 AAB77140	AAX37 AAX37 AAX895 AAX807 AAX10 2 AAX10 2 AAX11 2 AAX57 AAX57 AAX57 AAX57
11189 11189 11189 11284 11183 11183 11183 11183 11183 11183 1	1885 2885 3385 6884 6884 6884 1187 993 993 993
88844444888888888888888888888888888888	00000000000000
	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
01104444444444444444444444444444444444	00000000000000000000000000000000000000

#### ALIGNMENTS

promoter; peptide-nucleic acid; cyclised; gene therapy; target; site-directed mutagenesis; introduction; protein transport. Rat ornithine transcarbamylase signal peptide. AAR90584 standard; Protein; 43 AA 95DE-1020815 94DE-4421079 (updated)
(first entry) WPI; 1996-041226/05. Seibel A, Seibel P; (SEIB/) SEIBEL P. DE19520815-A1. 16-JUN-1994; 11-JUN-1995; 25-MAR-2003 31-0CT-1996 21-DEC-1995. Synthetic. AAR90584; AAR90584 

```
Synthetic.
                                                                                                                            nvention
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                         AAB18445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome
                                                                                                                                                                                                                                                                                                  RESULT 3
    ************
                                                                                                                                                                                                                                                                                                                                                          ά
                                                                                                                                                                                                                                                            셤
                                              Two modified oligonucleotides (introducing PstI and XhoI sites) were used to amplify a region of the human mitochondrial (mt) genome contg. the light strand promoter, mtDNA ori of the heavy strand, CSB's ("conserved sequence blocks") and a regulation site for DNA replication. Behind this fragment (5' direction) a synthetic multiple cloning site was introduced, generating a product with overhanign ends. The synthetic region also introduced a bidirectional mt transcription termination sequence. The amplification product, synthetic fragment and pBluescript were ligated and recombinant plasmid (AATISIS) was produced. Human mt is rank (differing from the native RNA only in having a modified nucleotide) was isolated by PCR from chloramphenicol resistant HeLa cloned inserted into plasmid 1 to form plasmid 2 (AATISIS). The cloned inserted sinto plasmid 1 to form plasmid 2 (AATISIS). Coloned inserted sequence). The cyclised using hairpin loop oligonucleotides, one of which carried the required signal peptide (the present sequence). The cyclised product was purified by treatment with exchucidease III. In a modification, the signal peptide was attached after cyclisation. The new plasmids were able to impart chloramphenicol resistance to otherwise sensitive B lymphocytes and fibroblasts. Similar plasmids without a signal peptide could not do this. The plasmids can be introduced into eukaryotic cells, esp. for site-directed mutagenesis or molecular therapy of genetic diseases, targeting nucleic mutagenesis or molecular therapy of genetic diseases, targeting nucleic coid in cells or their organsless will the protein transport route.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A recombinant vector for expressing a fused protein, useful for decomposing an extranuclear gene of a nonhuman organism -
                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                             Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ornithine transcarbamylase; MOT; fusion protein; extranuclear gene.
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 217; DB 17; 100.0%; Pred. No. 3.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat ornithine transcarbamylase signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
and molecular therapy of genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TANA/) TANAKA M.
(GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
                          Disclosure; Column 11; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 3; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG30857 standard; Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-2000; 2000JP-0380975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-2000; 2000JP-0380975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
vector; f
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-569946/61
                                                                                                                                                                                                                                                                                                                                                                                43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK88419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2002176988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; signal recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG30857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG30857
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leber hereditary optic neuropathy; myoclonic epilepsy;
neurogenic muscular weakness; ataxia; retinitis pigmentosa;
Kearns-Sayre syndrome; Leigh syndrome; Pearson Marrow pancreas syndrome;
aminoglycoside-associated deafness; diabetes; deafness; leukodystrophy;
hypotonia; autism; sudden infant death syndrome; hypoglycemia; leukaemia;
thrombocytopenia; migraine; hearing loss; stroke;
refractory infantile reflux; carnitine deficiency; multiple sclerosis;
blindness; optic atrophy; renal tubular acidosis; cardiomyopathy;
chronic pancreatitis; ATPase 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a method for functionally complementing one or more defects, mutations, or deletions in a mitochondrial genome of a cell having a nuclear genome. The method is used for treating a disease or disorder that arises from deletion of the protein-encoding genes of the mitochondrial genome. Alternatively, the method is used for treating a disease or disorder that arises from one or more defects, deletions or
The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence of a restriction enzyme recognishing a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism. The present sequence represents the signal peptide of rat mitochondrial periods of the contrained to the vector of the contrained to the contrai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functionally complementing one or more defects, mutations, or deletions in a mitochondrial genome of a cell, useful for treating diabetes with deafness, comprises introducing mitochondrial DNA into the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrial genome; mitochondrial encephalmyopathy; lactic acidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159; DB 23;
Pred. No. 2.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MISNIFILINKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by plasmid pUOATP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB18445 standard; Protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.3%; Soc
Best Local Similarity 100.0%; P:
Matches 32; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US06037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0123336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zullo SJ, Eisenstadt JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-565602/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA75084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200053773-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000,
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
AAR48260
ID AAR4
XX
AC AAR4
XX
DT 25-M
DT 29-J
                                                                                                                                                                                                                                                                                             ឧឧឧ
                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             쉽
                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
cc franscription and translation in the mitochondria. The diseases or disorders that can be ameliorated are mitochondrial encephalmyopathy with classifications and stroke-like episodes, Leber hereditary optic lattic acidosis and stroke-like episodes, Leber hereditary optic concurpathy, myoclonic epilepsy with ragged-red fibres, neurogenic muscular weakness, ataxia, retinitis pigmentosa, Kearnas-Sayra syndrome, classing adafiness, diabetes with deafness, leukodystrophy with hypothonia, autism with seizures, sudden infant death syndrome with hypothoria, autism with maternally inherited thrombocytopenia, hypothoria, leukaemia with maternally inherited thrombocytopenia, hypothoremia, leukaemia with maternally inherited thrombocytopenia, comigraines (associated with hearing loss, strokes, or diabetes), early hearing loss, refractory infantile reflux with cannitine deficiency, multiple sclerosis with seizures, blindness with optic atrophy and convalvular hypertrophic cardiomyopathy before age 50 and chronic pancreatitis with stroke-like episodes. The present sequence is encoded by plasmid pUOATP2. Plasmid pUOATP2 comprises a mutant oligomycinresistant ATPasse 6 mitochondrial gene derived from Chinese hamster ovary (CHO) cells linked to ornithine transcarbamylase DNA sequence. It is
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence of a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A recombinant vector for expressing a fused protein, useful for decomposing an extranuclear gene of a nonhuman organism -
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ornithine transcarbamylase; MOT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; signal peptide; ornithine transcarbamylase; MOT recombinant vector; fusion protein; extranuclear gene.
                                                                                                                                                                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                           MLFNLRILLNNAAFRNGHNFMVRNFRCGOPLOMNENL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ornithine transcarbamylase signal peptide.
                                                                                                                                                                                                                                                                                                                                                   50.2%; Score 109; DB 21
62.2%; Pred. No. 2e-08;
iive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZH GIFUKEN KOKUSAI BIO KENYUJO.
ZH OYO SEIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 3; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG30856 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-2000; 2000JP-0380975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-2000; 2000JP-0380975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 62.2 les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-569946/61.
N-PSDB; ABK88418.
                                                                                                                                                                                                                                                                                                                        258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TANA/) TANAKA M.
(GIFU-) ZH GIFUKE:
(OYOS-) ZH OYO SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2002176988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-2002.
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG30856;
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
peptide of human mitochondrial
be used in the vector of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for preparing a protein which interacts with the heat shock protein HSP47. The method involves the two-hybrid screening method using the HSP47 gene and a mammallan cDNA library. The HSP47 interacting proteins are useful for the diagnosis and treatment of diseases caused by an increase or decrease in activity of HSP47. The present sequence was used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Using the two-hybrid screening method to prepare proteins which interact with the heat shock protein \mbox{HSP47}
                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
                                                                                                                     Length 32;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat shock protein interacting protein; HSP47; OTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105; DB 22;
Pred. No. 6.4e-09;
2; Mismatches 8;
                                                                                                                     Score 108; DB 23;
Pred. No. 2.2e-09;
                                                                                                                                                                                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
  The present sequence represents the signal ornithine transcarbamylase (MOT) which may
                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 12; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                      AAG64224 standard; Peptide; 32 AA
                                                                                                                                                           ,;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR48260 standard; peptide; 32
                                                                                                                     49.88;
68.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0330631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0330631
                                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTC peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-395263/42.
                                                                                                                                  Local Similarity
les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP2001145493-A.
                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
29-JUL-1994
                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                AAG64224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR48260;
                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                   Query Match
```

```
Intracellular binding to a desired target by an intracellularly corpressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMS), so that the expression of multiple major histocompatibility (MHC) can locules is blocked. This selective targeting of IRMS, their pathways or components, can be used to selectively regulate the immune system by controlling expression of these molecules and immune system by controlling expression of these molecules and of the MHC pathway or the MHC assembly line or antigen presentation of the AHC pathway or the MHC assembly line or antigen presentation can be targeted. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for transplantation can be perfused with the intrabody ex vivo. The intrabodies can comprise whole antibodies, heavy chains, Fab' fragments, single-chain antibodies, heavy chains, Fab' also comprise an intracellular localisation signal to facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interception of expressed proteins. For example, if the target was a cell surface receptor, the antibody would comprise a leader sequence and an endoplasmic reticulum (ER) or Golgi apparatus retention signal. This peptide is a localisation sequence for the mitochondrial matrix. For other localisation sequences see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Localisation sequence to direct antibodies to the mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB 20;
Pred. No. 6.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                             Altering the regulation of the immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                         amino acid"
                                                                                                                                                       /note= "Any amino acid"
                                                                                          /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                               (DAND ) DANA FARBER CANCER INST INC.
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 28; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG92993 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.48;
                                                                                                                         /note- "Any
                                                                                                                                                                                                                                                  98WO-US19563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                             Marasco W, Mhashikar A;
 endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-229546/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 AA;
                                                                                                          Misc-difference
                                                                            Misc-difference
                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW96345-W96377
                                                                                                                                                                                       WO9914353-A2
                                                                                                                                                                                                                                                  18-SEP-1998;
                                                                                                                                                                                                                                                                                 19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2002
                                                                                                                                                                                                                     25-MAR-1999
                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG92993
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXEXEXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New vector systems comprise a sequence adapted for intracellular delivery and expression contg. a promoter operably linked to an antibody gene encoding an antibody which binds to a specific target antigen. The antibody is esp. a single chain antibody in which the heavy and light chain variable regions are joined via a hydrophilic linker peptide. Localisation sequences are pref. included in the constructs. The sequence AAR48260 is a mitochondrial matrix retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intracellular binding of antigens - by using antibody targetting with vector system, for e.g. tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; immune response; modulation; MHC; IRM; receptor; intrabody; major histocompatibility complex; graft rejection; immunomodulatory response molecule; regulation; transplantation; retention signal; localisation signal; golgi apparatus; ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                           Single chain antibody; sFv; heavy chain; light chain; variable domain; hydrophilic linker; antibodies; targetting; subcellular localisation signal; mitochondrial matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrial matrix localisation signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 15;
Pred. No. 6.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
             Mitochondrial matrix retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 103; 155pp; English
                                                                                                                                                                                     'note= "not defined"
                                                                                                                                                                                                                   'note= "not defined"
                                                                                                                                                                                                                                                                                                                                                                                                                        (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                  /note= "not defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96358 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.48;
                                                                                                                                                                                                                                                                                                                                                                          92US-0916939.
                                                                                                                                                                                                                                                                                                                                             93WO-US06735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haseltine WA, Marasco WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-048868/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 19; Conserva
                                                                                                                                                                      Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AA;
                                                                                           retention signal
                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                              WO9402610-A1
                                                                                                                                                                                                                                                                                                                                             16-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1992;
17-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1999
                                                                                                                                                                                                                                                                                                              03-FEB-1994
                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW96358
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ö

Gaps

; 0

Length 32; 10; Indels

```
Sequence
```

Regulator; transcription; cell death; phenotype; molecular scaffold; gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure; ischaemia; obesity; neurodegenerative disease; Alzhehmer's disease; bone pathology; dermatologic disease; psoriasis; infection; AIDS; acquired immunodeficiency syndrome; cosmettc; wound healing; antibiotic transport; drug toxicity; drug resistance; immunobiology; inflammation; allergic response; human immunodeficiency virus. Identifying regulator polypeptides which influence target transcriptional regulatory regions, useful for treating cancer, comprises introducing host cells expressing the polypeptide into a library of polynotectides. Disclosure; Page 37; 224pp; English. 2001US-265589P. 2001US-265880P. 2001US-271423P. 2001US-263226P. 2000US-192586P. 97US-935377P. 04-FEB-2002; 2002WO-US02814 (UYRP ) UNIV ROCHESTER. Smith ES; WPI; 2002-643398/69. WO200262822-A2. Unidentified. 02-FEB-2001; 23-JAN-2001; 28-MAR-2000; 22-SEP-1997; 27-FEB-2001; 15-AUG-2002 Zauderer M,

The invention discusses a method for identifying polynuclectides encoding transcriptional regulatory region in a host cell. The method comprises providing a population of eukaryotic host cell. The method comprises polypeptide, introducing into the host cell a library of polynuclectides and the recovering them from the host cells. The target transcriptional regulatory region is operably associated with a polynuclectides and then recovering them from the host cells. The target transcriptional regulatory region is operably associated with a polynuclectide encoding a gene product, the expression of which results in host cell death or cause the host cells to exhibit a pre-determined modified phenotype and where the gene product is expressed upon activation of target transcriptional regulatory region. Each candidate modified phenotype and where the gene product is expressed upon activation of target transcriptional condidate peptide is displayed on the surface of the candidate regulator candidate peptide. The methods are useful in selecting and/or screening confidence or suppress the transcriptional activation of a target transcriptional regulatory region in a encaptic host cell. These capulator molecules may be used (e.g. in gene therapy) for preventing or transcriptional regulatory region in a encary, cardiovascular diseases (e.g. arrhythmia, heart failure, isonemia cancer), cardiovascular diseases (e.g. arrhythmia, heart failure, isonemia, obesity, neurodegenerative consistence (e.g. arrhythmia, near failure, isonemia, obesity, neurodegenerative consistence (e.g. arrhythmia, heart failure, isonemia egolistor molecules that block and in subconfices and in wound imminger than annications and in wound in a enterpress and in insertions and in insertions and in insertions and in insertions a resistance applications and in improving the performance of existing or developmental drugs. It may also be used in immunobiology, inflammation, allergic response and in biotechnology applications. The sequences presented in ABG92946-ABG93029 are examples of regulator polypeptides. The invention discloses a method for identifying polynucleotides 32 AA;

```
ö
                                 Gaps
                                ö
 Score 92; DB 23; Length 32;
Pred. No. 6.8e-07;
2; Mismatches 10; Indels
42.4%;
ilarity 61.3%;
Conservative
Query Match
Best Local Similarity
Matches 19; Conserve
```

The present invention describes a method for selecting polynucleotides (PNs) encoding an intracellular immunoglobulin molecule or its fragment whose expression induces a modified phenotype in a eukaryotic host cell (I). The method comprises introducing into (I) a first and second library of PNs encoding, through operable association with a transcriptional control region, first and second intracellular immunoglobulin subunit polypeptides, respectively. The method is useful for selecting polynucleotides which encode an intracellular immunoglobulin molecule, or fragment. The method is useful e.g. for identifying polynucleotides which singly or collectively encode intracellular immunoglobulin molecules, or which sensitise host cells to killing by an agent. The method may also be used in cardiovascular applications; for screening for diminished

arrhythmia potential in cardiomyocytes and for enhanced contractile properties of cardiomyocytes and diminish heart failure potential; for identifying intracellular immunoglobulin molecules that will regulate intracellular and sarcolemmal calcium cycling in cardiomyocytes to prevent arrhythmias or that will diminish embolic phenomena in arteries

```
Identification; intrabody; eukaryotic cell; immunoglobulin; selection; cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke; enhanced contractile property; heart failure; arrhythmia; embolic; sarcolemmal calcium cycling; artery; arteriole; angina; atherosclerosis; LDL metabolism; skin biology; keloid formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selecting polynucleotides encoding an intracellular immunoglobulin which induces a modified phenotype in a eukaryotic host cell, by introducing library of polynucleotides encoding immunoglobulin subunit polypeptides.
                                                                                                                                       Mitochondrial matrix targeting peptide SEQ ID NO:54.
  31
                   1 MLENLRXXLNNAAFRHGHNFMVRNFRCGOPL 31
MLSNLRILLNKAALRKAHTSMVRNFRYGKPV
                                                                                                                                                                                                                                                                      /note= "any amino acid"
                                                                                                                                                                                                                                                                                           'note= "any amino acid"
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYRP ) UNIV ROCHESTER MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 44; 257pp; English.
                                                                            Ź
                                                                                                                                                                                                                                                                                                                 /note= "any amino
                                                                       ABP56588 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                     2001US-263225P.
2001US-263200P.
2001US-271422P.
                                                                                                                                                                                                                                                                                                                                                                                                                                      L5-JUN-2001; 2001US-298095P
                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2002; 2002WO-US01677
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wei C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-103408/09.
                                                                                                                                                                                                                                                                                Misc-difference 8
                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                          Identification;
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                    WO200286096-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2001; 2
24-JAN-2001; 2
27-FEB-2001; 2
                                                                                                                   24 - MAR - 2003
                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sauderer M,
                                                                                   ð
                 pp
```

ä

ö

```
and arterioles leading to strokes and angina; in screening for decreases in a therosclerosis producing mechanisms to find intracellular immunoglobulin molecules that regulate LDD and HDL metabolism; in skin blology applications; and in regulating or inhibiting keloid formation. AB222379 to ABZ22449 and ABP56536 to ABP56618 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a localisation sequence that can be used to direct stabilised single-chain antibodies to the mitochondrial matrix. The N-terminus of the single-chain antibody is linked to a stabilising fusion peptide, referred to as a stabilon, which increases stability of may be modulated by linking the stabilon, which increases stability of may be modulated by linking the stabilon to the antibody through a protease-sensitive linker region. The stabilon is removed upon induction of expression of a specific restriction protease by means of an inductible promoter, and this renders the antibody susceptible to protecolysis by the N-end rule pathway. This method for regulating protein stability allows removal of the antibody after it has bound to its target antigen. Stabilised recombinant proteins may be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrial matrix localisation sequence; single-chain antibody; stabilon; stabilising fusion peptide; vaccine; gene therapy; protein degradation modulation; protein stability; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating degradability of protein or peptide useful for gene therapy involving antibodies, comprises altering a gene at the N terminus to render protein or peptide metabolically stable -
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   ö
                                                                                                                                                               Length 32;
                                                                                                                                                                                               10; Indels
                                                                                                                                                          Score 92; DB 24;
Pred. No. 6.8e-07;
2; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "unspecified amino acid"
                                                                                                                                                                                                                           1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                       1 MIFNERXXINNAAFRHGHNFMVRNFRCGOPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrial matrix localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOPHARMACEUTICALS USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 50; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                  AAB15704 standard; Peptide; 31 AA
                                                                                                                                                            42.48;
61.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2000; 2000WO-US00558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0115505
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                        Query Match
Best Local Similarity 61.3 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MIND-) MINDSET BIOP
(MCIN/) MCINNIS P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-476059/41.
                                                                                                                        32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200042185-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                        08-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2000
                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                     AAB15704:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chain DG;
                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                 AAB15704
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                          g
```

```
The invention relates to a controlled release drug delivery system.

Target cells in a patient are transformed with an expression construct encoding an antibody (particularly a single chain antibody) to the drug to be delivered. The antibody contains a modulator of intracellular half-life; this can either be a stabilising or destabilising residue located in the N-terminus after the initial methicule, or a peptide ("stabilon") containing a stabilising residue linked to the antibody of the antibody but a protease cleavage site. On administration of the drug, the antibody binds the drug, localising it at the target cells but maintaining it in an inactive state. As the antibody is degraded (the timescale for which is dependent upon the N-terminal or stabilon amino caids), the drug is released at its site of action where it can exert its effects. The antibody encoded by the expression construct (and therefore the therapeutic agent) can be targetted to particular such as such as the noclaus by including the appropriate cellular localisation signals. The novel method may be used to deliver therapeutic agents to the variety of conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                               Controlled release delivery system; drug targetting; drug-specific antibody; intracellular half-life; gene therapy; diabetes; autoimmune disease; inflammatory disease; infectious disease; cancer; side effect; subcellular localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delivering a drug, to a patient suffering from cancer or diabetes, at a predetermined site, comprises altering a target cell to express a drug specific antibody by gene therapy and administering the drug -
                                                                                                            Gaps
therapy for the treatment of disorders such as Alzheimer's disease
                                                                                                              ä
                                                                         Length
                                                                                                          Indels
                                                                     Score 79.5; DB 21;
Pred. No. 5.8e-05;
; Mismatches 10;
                                                                                                                                                                        1 MLFNLR-XLNNAAFRHGHNFWYRNFRCGGPL 30
                                                                                                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MIND-) MINDSET BIOPHARMACEUTICALS USA INC
                                                                                                                                                                                                                                                                                                                                                                              Mitochondrial matrix localisation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 44; 69pp; English.
                                                                                                                                                                                                                                                                  AAB22835 standard, peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= unknown
Misc-difference 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- unknown
                                                                     36.6%;
61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000WO-US04749.
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-572044/53.
                                                                                       Similarity
                                    31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200050089-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                           10-JAN-2001
                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-2000
                                    Sequence
                                                                                                                                                                                                                                                                                                        AAB22835;
                                                                   Query Match
                                                                                       Local
                                                                                                      Matches
                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                     õ
```

```
2000US-0235484.
2000US-0235834.
2000US-0235836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0237040
2000US-0239935
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0229513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0231242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000US-0231243
000US-0231244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0231413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000US-0231414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000US-0232080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0231968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0232398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000US-0232399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0233064
2000US-0233065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0236367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0236369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0236370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0237037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0237039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0240960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0241221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0241785
2000US-0241786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0241809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20000S-0241826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0232081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000US-0232401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000US-0233063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0234223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0236327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0239937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000US-0241787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0246526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000US-023427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-0CT-2000;
20-0CT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2000;
01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-0CT-2000;
diabetes, autoimmune diseases, inflammatory diseases, infectious diseases and especially cancer. The delivery method of the invention causes a drug to become almost immediately localised at lits site of action in an inactive form where it accumulates. Once released by antibody degradation, the drug is at an effective concentration only at the target site, with very little free drug being available in the rest of the body. The system of the invention therefore reduces the side effects caused by therapeutic agents, and also provides economic benefits as a smaller amount can be administered to the patient. Sequences hab22837 and ABD22837 and ABD22837 and also provides economic benefits sequences which can incorporated into a drug-specific antibody used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, oxidoreductase enzyme; transferase; hydrolase; lyase; lsomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; organical disorder; nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
36.6%; Score 79.5; DB 21; Length 31;
Best Local Similarity 61.3%; Pred. No. 5.8e-05;
Matches 19; Conservative 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human enzyme polypeptide #554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU23468 standard; Protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200005-0180528
200005-018664
200005-018934
200005-018934
200005-0189874
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
200005-020515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US01239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0225267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                      31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-2000;
02-MAR-2000;
17-MAR-2000;
18-APR-2000;
18-APR-2000;
19-MAY-2000;
20-JUN-2000;
20-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 - JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2000;
34-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU23468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A CONTRACTOR OF THE PROPERTY O
```

3,

```
The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the unctional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. avicentials), returned the prevention and/or prognosis of a wide range of immunodeficiency disorders (e.g. Alzheimer's disease), e.g. arthmitis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atharosclerosis), blood-related disorders (e.g. thempophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.

AAUZ2915-AAUZ3814 represent the novel human enzyme polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID No 1464; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0250391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000; 2000US-0256719
06-DEC-2000; 2000US-0251479
08-DEC-2000; 2000US-0251856
08-DEC-2000; 2000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-465566/50.
N-PSDB; AAS41338.
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000;
01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38-DEC-2000;
                                                                                                                                                                                                                 17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                            NOV-2000;
                                                                                                                                                                                                                                                                              17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases
```

```
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                   Gaps
                                                                                                                         52 LRMTLOKESAMIARSRKPHATMIRNAKYSGLHAGWSLWLPVESALQSHQPR 102
                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                              5 LRILLNK-----AALRKAHTSMVRNFRYG------KPVQSQVQL-KPR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                 15;
                                      Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 15; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|| ||: :|| :: :|| :| :|| :| |:|| :: :|| |:|| 613 LTNLHILI------SHIDLMEDFHRFGRNLYEPVAYRLGWEPRD 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSNLRILLNKAALRKAHTSMVRNF-RYGK----PVQSQVQLKPRD 41
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                      DB 22;
                                                                 11;
                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.9%; Score 54; DB 22; 33.3%; Pred. No. 33; 1ve 11; Mismatches 7
                                    Score 56.5; DE
pred. No. 1.6;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                      ABB57741 standard; Protein; 866 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                      26.0%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.38
Matches 15; Conservative
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL01844.
                                                       Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                866 AA;
           149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interactions
                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                  ABB57741;
           Sequence
                                      Query Match
                                                                                                                                                                           RESULT 13
                                                                                                                                                                                         ABB57741
                                                                                                                                                                                                                      ö
X X
                                                                                                 δ
                                                                                                                              g
```

ë,

RESULT 14

```
Search completed: July
Job time : 38.881 secs
           WO9909186-A2
                                                           14-AUG-1998;
                                                                                            14-AUG-1997;
                                   25-FEB-1999
                                                                                                                                                       Guigueno A;
                                                                                                                                            Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                          Sequence
 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉽
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0180-ABL16175) and the encoded proteins (ABB7737-ABB72072).

(ABB57737-ABB72072).

The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 4569; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 4569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.7%; Score 53.5; DB 22; 10.2.5%; Pred. No. 33; Conservative 5; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LSNLRILLNKAALRKAHISMVRNFRYGKPVQSQVQLKPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium species protein sequence 38B.
                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
           ABB59259 standard; Protein; 755 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY04933 standard; Protein; 165
                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                                                           (first entry)
                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              755 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL03362
                                                                                                                     pharmaceutical.
                                                                                                                                                                 WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                     interactions -
                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999
                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY04933;
                                   ABB59259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
ABBS9259
ID ABBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY0493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                                                                                                                                         Goguet de la Salmoniere Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                              · for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 165;
                                                                                                                                                                                                                                                                                                                                Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::| | |||: | | | :|: | 119 RVILRCAHTRKANQSRARTLRPLRPL--RIALRPR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.0%; Score 52; DB 20; 37.1%; Pred. No. 8.9; iive 8; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPR 40
                                                                                                                                                                         Portnoi D,
                                                                                                                                                                                                                                                                                                                                                                                    infection-associated protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24, 2003, 22:04:08
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 32; Fig 38B; 309pp; French
                                                                                                                                                                         Pelicic V,
98WO-FR01813,
                                             97FR-0011325.
97FR-0010404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                         (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                            Lim EM,
                                                                                                                                                                                                                                                     WPI; 1999-181045/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA;
                                                                                                                                                                                                                                                                             N-PSDB; AAX34186
```